

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 05:47:40 ; Search time 1870.66 Seconds
(without alignments)
14318.993 Million cell updates/sec

Title: US-09-970-624-1
Perfect score: 1280
Sequence: 1 gccacgagccgcctgcgcc.....aaaaaaaaaaaaaaaa

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank! :
1: gb_ba :
2: gb_htg :
3: gb_in :
4: gb_om :
5: gb_ov :
6: gb_pat :
7: gb_ph :
8: gb_pl :
9: gb_pr :
10: gb_ro :
11: gb_sts :
12: gb_sy :
13: gb_un :
14: gb_vi :
15: em_ba :
16: em_fun :
17: em_hum :
18: em_in :
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24: em_ph :
25: em_pl :
26: em_ro :
27: em_sts :
28: em_un :
29: em_vi :
30: em_htg_hum :
31: em_htg_inv :
32: em_htg_other :
33: em_htgo_inv :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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1	1109.6	86.7	1268	6	AX085151	AX085151 Sequence
2	1109.6	86.7	1268	6	AX085348	AX085348 Sequence
3	1109.6	86.7	1268	8	AF112149	AF112149 Zea mays
4	463.4	36.2	5031	6	AX085162	AX085162 Sequence
5	463.4	36.2	5031	6	AX085359	AX085359 Sequence
6	290	22.7	936	6	AMDEPH125	Y10750 A.majus mRN
7	265.6	20.8	687	8	AF336979	AF336979 Arabidops
8	254.8	19.9	775	8	MSU91964	U91964 Medicago sa
9	249.6	19.5	916	8	AF312662	AF312662 Arabidops
10	245	19.1	310	6	AX085160	AX085160 Sequence
11	245	19.1	310	6	AX085357	AX085357 Sequence
12	239.4	18.7	1098	6	ATU20186	Z97057 Arabidops
13	236.4	18.5	801	8	AF099937	U20186 Arabidops
14	208.6	16.3	1039	8	AF396746	AF396746 Ipomoea b
15	176.8	13.8	1061	8	AF099937	AF099937 Hyacinthu
16	174.4	13.6	251	6	AX085161	AX085161 Sequence
17	174.4	13.6	251	6	AX085358	AX085358 Sequence
18	172.8	13.5	1355	6	PMU69483	U69483 Picea maria
19	172.8	13.5	1642	8	PMU46582	U46582 Picea maria
20	172.8	13.5	1726	8	AF006210	AF006210 Pinus res
21	171.2	13.4	922	8	AF023615	AF023615 Pinus rad
22	171.2	13.4	1657	8	PMU69482	X79280 P.abies dal
23	171.2	13.4	1753	8	PADAL2	U69484 Picea maria
24	167.6	13.1	1212	8	PMU69484	AF234617 Phalaenop
25	165.8	13.0	1009	8	AF234617	AF088956 Sequence
26	165.8	13.0	1043	6	AR088956	U78782 Oryza sativ
27	165.8	13.0	1043	8	OSU78782	U31522 Zea Mays MA
28	165.2	12.9	1069	8	ZMU31522	AJ132209 Gnetum gn
29	164.8	12.9	1154	8	GGN132209	AJ251118 Malus dom
30	163.4	12.8	1037	8	MDO251118	L18924 Corn ZAGI m
31	161	12.6	1351	8	MEZ2AC1A	AL606460 Oryza sat
32	159.8	12.5	174264	2	OSJN00003	Z46612 P.ginseng v
33	159.4	12.5	1080	8	PGORF6AG2	AJ249145 Hordeum v
34	158.4	12.4	984	8	HVU249145	X81852 P. hybrida
35	158.4	12.4	999	8	PHEBP11	L46397 Zea mays MA
36	157.6	12.3	1262	8	MEZEMADSA	AB003324 Oryza sat
37	157.2	12.1	1175	8	AB003324	AJ249142 Hordeum v
38	155	12.1	861	8	HVU249142	AJ249141 Hordeum v
39	155	12.1	1086	8	HVU249141	AJ271208 Zea mays
40	152.4	11.9	1039	8	ZMA271208	AJ132207 Gnetum gn
41	151.6	11.8	1170	8	GGN132207	AB003328 Oryza sat
42	151.4	11.8	1095	8	AB003328	AB007505 Trilicium
43	151	11.8	1176	8	AB007505	U31521 Zea mays MA
44	150.8	11.8	1083	8	ZMU31521	AF151693 Oryza sat
45	150.6	11.8	1193	8	AF151693	

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	BASE COUNT	ORIGIN
1	AX085151	Sequence 1 from Patent WO0112798.	AX085151	AX085151.1	GI:13275244			1268 bp	DNA	linear	PAT 09-MAR-2001		360 a	298 c

1 (bases 1 to 1268)
Loerz,H., Dresselhaus,T., Schreiber,D. and Heuer,S.
Male sterile plants
Patent: WO 0112798-A 1 22-FEB-2001;
Suedwestdeutsche Saatnucht (DS)
Location/Qualifiers
1..1268
/organism="Zea mays"
/db_xref="taxon:4577"

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 Qy 671 agaaatattcgcagctgacggagagatgatcttcttgaggcttgatgcaagaactgca 730
 Db 594 AGAAATATTATGGCAGTTTGACGGAGATGATCTTCTGGGCTGATGATCAAGAACTGCA 653
 Qy 731 gtccctggagaatcaattggaacaagcctgctgctgctgctgctgctgctgctgctgct 790
 Db 654 GTCCCTGGAGATCAATTGGAACAAGCTGCTGGTGTCCGCCAAGAAAGACCATCT 713
 Qy 791 ctgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 850
 Db 714 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 773
 Qy 851 agactgtgacataagatacaaccctgctgctgctgctgctgctgctgctgctgctgct 910
 Db 774 AGACTGTGACATAAGATCAACCTGATTCGCCAAGAAATGATGATGATGATGATGATGAT 833
 Qy 911 atatgagactgaaagacccaagtgagtgatlaalcggagagtcacccgactcattcact 970
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 Qy 971 agtagtgaaacccaagatgttctgtgcaactggaactgaacactgcaacactgcaacaa 1030
 Db 894 AGTAGTGAACCAAGAGATGTTCAGTGGCAACTTGAACCTCAGCACTGCGCAACAA 953
 Qy 1031 taactatgagccactactgctcctcctcctcctcctcctcctcctcctcctcctcctc 1090
 Db 954 TAACATTGAGCGCATCTACTGCTCTAGCTAGGATTTGCAATTATTCATGAAAGAGAGT 1013
 Qy 1091 aaaactgcgtctctatgagtctggaagaaacttattatggaagagatgatactagag 1150
 Db 1014 AAAACTGCGCTCTATGATCTGAAAGAACTATTATTTGTAAGAGATGATCTCAGAG 1073
 Qy 1151 aaagacatcttgagcagagagatitgagatlatgaaactataatgataatgataat 1210
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 Qy 1211 ttccaagccggaatggggtcgtggaattcagagagatgattgcttcta 1258
 Db 1134 TTTCAGACTGGAATGGGGTGTGGAATTCAGAGATGATGCTTCTTA 1181
 RESULT 4
 AX085162 5031 bp DNA linear PAT 09-MAR-2001
 LOCUS AX085162
 DEFINITION Sequence 12 from Patent WO0112798.
 ACCESSION AX085162
 VERSION AX085162.1 GI:13275254
 KEYWORDS
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 5031)
 Loerz,H., Dresselhaus,T., Schreiber,D. and Heuer,S.
 Male Sterile Plants
 Patent: WO 0112798-A 12 22-FEB-2001;
 Suedwestdeutsche SaatZucht (DE)
 Location/Qualifiers
 1..5031
 /organism="Zea mays"
 /db_xref="taxon:4577"
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 2871..2954
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 3202..3258
 /note="EXON III"
 4066..4166
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 4248..4289
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 exon
 exon

Query Match 36.2%; Score 463.4; DB 6; Length 5031;
 Best Local Similarity 96.5%; Pred. No. 1.4e-96;
 Matches 518; Conservative 0; Mismatches 11; Indels 8; Gaps 4;
 BASE COUNT 1555 a 1006 c 929 g 1541 t
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 Qy 6 agcgcgcctgcgcgaagaaagccatgcttctcccaacaacgcaacatagaacatca 65
 Db 1465 ATCCGCCCTGCGCCCAAGAAAGCCATCTGTTCCACAAAGCAGACATAGAAAGATCA 1524
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 Db 1525 TTCCCTCTCGGCTAGCTTCTCTC--CTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCT 1582
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 Qy 185 ctccctactcttcttggacgcttgcggcgcgcgcggaagaagatagatcccgacatcg 244
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 Qy 245 tgcgtcgtcctccttgccttcgcagtcgagggcgcaacacacactcgcctcctatgagc 304
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 Qy 305 tgcgaagcgagcaagggtcgaagaagagctagctatagagcggaagatcgatgg 364
 Db 1762 TCGCGCGCGAGCCAGGGTCAAGAAAGAG---AGCTAGCTATAGGCGGAGATGATGG 1817
 Qy 365 gagggaaagatcgtgacccgacagatgataactccacggcgagggagactctc 424
 Db 1818 GAGGGGAAAGATCGTGCATCCGAGATGATTCACGAGCGGAGGAGGACTCTCTC 1877
 Qy 425 caagcgcggaacggagatcttcaagaagccaagagagctgcacatcctctgcagtcgga 484
 Db 1878 CAAGCGCGGAAACGGAGATCTTCAAGAAAGCCAGAGCTGCCATTCGATGGGGA 1937
 Qy 485 gtcggtcgtgctatcttctccagacccggcgccctttagagtaacttagaccag 541
 Db 1938 GTGCGCCTCGTCACTTCTCAGACCGCGCGCTCTTACAGATGATGACACACAG 1994
 RESULT 5
 AX085359 5031 bp DNA linear PAT 09-MAR-2001
 LOCUS AX085359
 DEFINITION Sequence 12 from Patent WO0112799.
 ACCESSION AX085359
 VERSION AX085359.1 GI:13275414
 KEYWORDS
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 5031)
 Loerz,H., Dresselhaus,T., Schreiber,D. and Heuer,S.
 Regulatory sequences for pollen specific or pollen abundant gene
 expression in plants
 Patent: WO 0112799-A 12 22-FEB-2001;
 Suedwestdeutsche SaatZucht (DE)
 Location/Qualifiers
 1..5031
 /organism="Zea mays"
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 exon /note="EXON V"
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 exon /note="EXON VI"
 4523..4676
 exon /note="EXON VII"
 BASE COUNT 1555 a 1006 c 929 g 1541 t
 ORIGIN

Query Match 36.2% Score 463.4; DB 6; Length 5031;
 Best Local Similarity 96.5%; Pred. No. 1.4e-96;
 Matches 518; Conservative 0; Mismatches 11; Indels 8; Gaps 4;
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 1465 ATCCGCCCTGGCCAGCAAGCAAGCATGCTCTCCCAACAGCAGACATAGAGCATCA 1524
 Db 66 ttccctctcgtagctctctctctctctctctctctctctctctctctctct 124
 1525 TTCCCTCTCGGCTAGCTCTCTC--CTCTCTCCCTCTCTCTCTCTCTCTCTCT 1582
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 Db 185 ctctctactctctcttgagcagctcgcgcgcgcgagagaagatagatccgcacatcg 244
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 1762 TCGCGCGCGCGAGCCAGGCTCAAGAGAG-AGCTAGCTATAGCCCGAGATGATGCGG 1817
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 1938 GGTGCGGCTCTGATCTCTCTCCAGCAGCGCGCGCTTACAGATCTAGCAGCAG 1994
 Db

RESULT 6

ANDEFH125 936 bp mRNA linear PLN 19-AUG-1997
 LOCUS A.majus mRNA for DEFH125 protein.
 DEFINITION Y10750
 ACCESSION Y10750.1 GI:1816458
 VERSION Y10750.1 GI:1816458
 KEYWORDS DEFH125 protein.
 SOURCE snapdragon.
 ORGANISM Antirrhinum majus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Lamiales; Veroniceae; Antirrhinum.
 REFERENCE 1 (bases 1 to 936)
 Authors Zaehgo, S., Saedler, H., and Schwarz-Sommer, Z.
 Pollen-specific expression of DEFH125, a MADS-box transcription

JOURNAL Factor in Antirrhinum with unusual features
 MEDLINE Plant J. 11 (5), 1043-1050 (1997)
 REFERENCE 97336298
 2 (bases 1 to 936)
 AUTHORS Schwarz-Sommer, Z.
 TITLE Direct Submission
 JOURNAL Submitted (23-JAN-1997) Z. Schwarz-Sommer, MPI fuer
 Zuechtungsforchung, Plant Molecular Genetics, Carl-Von-Linne-Weg
 10, D-50829 Koeln, FRG

FEATURES

source Location/Qualifiers
 1..936
 /organism="Antirrhinum majus"
 /db_xref="taxon:4151"
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 /codon_start=1
 /product="DEFH125 protein"
 /protein_id="CAA71739.1"
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 /translation="MGRKIVQRIIDKSTSRQWTFPSRRSGILKKAKELALCDAAEVG
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CDS

BASE COUNT 317 a 160 c 216 g 243 t
 ORIGIN

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 Best Local Similarity 64.4%; Pred. No. 1.4e-56;
 Matches 434; Conservative 0; Mismatches 240; Indels 0; Gaps 0;

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 Db 419 ctctccaagcgcgcgaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 478
 75 TTTTTCGAAAAGAGGAGTGACCTTTGAAGAGGCCAAGAGCTGCTATCTTTGTGA 134
 QY 479 tgcgagagtcgctcgtcactctctctcagcagcagcagcagcagcagcagcagcagcagc 538
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 Db 539 cagcagaaatcagctgtagatcgtacgcagcagcagcagcagcagcagcagcagcagcagc 598
 195 CAGCATGAATCATTTTGTAGCAGCACACTAAACCAAGAGACATCATCATCGCT 254
 QY 599 aaatcccaactcgagccttaagcttggcagaagagagcagcagcagcagcagcagcagc 658
 255 TAATCATGCTCGGAGAGCTCAAGTTTGGCAAGGAGGAGCTGCACTTTAAGGCAACATT 314
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 495 TCAAGCAGCAATATGAGCTTATGAGAGAGTAAACTCTTCAACAAAGAAAGAGAAATT 554
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 555 GTGTAAAGAGCTTACGAGCAAGGAGATGTAAAGTGAAGCAATGAGACTGCTTGTTC 614
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Db 615 ATTTGTTTTCGCAATTCGTAGGACAAATTCAGCCAAATCCAGCTTCATTTAAGCCAGCC 674
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RESULT 7
AF336979 687 bp mRNA linear PLN 02-FEB-2002
LOCUS Arabidopsis thaliana MADS-box protein AGL21 mRNA, complete cds.
ACCESSION AF336979
VERSION AF336979.1 GI:18478602
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 687)
Burgel, C., Liljegren, S.J., Yanofsky, M.F. and Alvarez-Buylla, E.R.
Alvarez-Buylla, E.R.
MADS-box gene expression in lateral primordia, apical meristems and
differentiated tissues of Arabidopsis thaliana roots
Unpublished
2 (bases 1 to 687)
Burgel, C., Liljegren, S.J., Yanofsky, M.F. and Alvarez-Buylla, E.R.
Direct Submission
Submitted (15-JAN-2001) Lab. Genetica Molecular y Evolucion,
Instituto de Ecologia, UNAM, Terceer Circuito Exterior, Anexo al
Jardin Botanico, Mexico City, DF 04510, Mexico
location/Qualifiers
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BASE COUNT 245 a 136 c 154 g 152 t
ORIGIN

Query Match 20.8%; Score 265.6; DB 8; Length 687;
Best Local Similarity 67.1%; Pred. No. 5.9e-51;
Matches 376; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

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OY 420 ttctccaagcgccggaagatcttccaagaagcgagcgatcgcatctctcgtgac 479
Db 61 TTCTCCAAACGAGAAAGGCTTATTCAGAAAGCCAAAGAGCTAGCTATTCCTGTGAT 120
OY 480 ggcgagatcgccctcgtatctcttccagacacgcccgcctctacgactctagacc 539
Db 121 GCCGAGTCGCGTCTCATCTCTCTCTGACACCGGAAAGCTCTATGACTTTGCAAGCTCC 180
OY 540 agcagaatacgtatagatcgatcgatcgagcgaagcgaagaagcgaagtcgtcgca 599
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OY 660 cacaactgcaagaatlatcgcagcttgacgagagatgactcttcctggcgtgaagtc 719
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OY 720 aagaactcgagctccctgagaaatcaatggaacaacgctgctgctgctgcgcaag 779
Db 361 AACGAGCTAAACAGTCTGAGAAATCAAAATGAGATTAAGTTGCGTGAATCTATGAGA 420
OY 780 aagagccatctctgatagatgagatcagatcagattgagatggaagcgcaagtttacc 839
Db 421 AAGGAAACACTGTTGACTCAAGAAATCCAAAGACTTAAGCCAAAGAGCAATCTTATTCAT 480
OY 840 caagaanaatacagactgtacataagaatcaactgtatgctccagaagaatgatgagta 899
Db 481 CAGGAAACCTGCAATTTATTCAGAAAGTACACGAGATTCATCAAGAAATGCTGAGCTC 540
OY 900 cataaagaatataatgagac 919
Db 541 TACAAGAAAGCTTATATGTC 560

RESULT 8
MSU91964 775 bp mRNA linear PLN 05-APR-1997
LOCUS Medicago sativa MADS-box protein mRNA, partial cds.
ACCESSION U91964
VERSION U91964.1 GI:1928873
KEYWORDS
SOURCE Medicago sativa.
ORGANISM Medicago sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
REFERENCE
1 (bases 1 to 775)
Dunn, K. and Heard, J.
Direct Submission
Submitted (04-MAR-1997) Biology, Boston College, 140 Commonwealth
Ave, Chestnut Hill, MA 02167, USA
location/Qualifiers
1..775
/organism="Medicago sativa"
/db_xref="taxon:3879"
/feature="located in infected cells of alfalfa root nodules;
evolutionarily related to agl 17"
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/product="MADS-box protein"
/protein_id="AB51377.1"
/db_xref="GI:1928874"
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BASE COUNT 283 a 128 c 179 g 185 t
ORIGIN

Query Match 19.9%; Score 254.8; DB 8; Length 775;
Best Local Similarity 69.0%; Pred. No. 1.9e-48;
Matches 349; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

OY 366 aggggaagaatcgtatccgcagagatcgaactccacgagcgagtgagcttctcc 425
Db 1 AGAGGGAAGATCCACAGATTAAGAGATAGAGACACACAGCAAGACAGTAATCTTTTG 60
OY 426 aagcgccggaagcgagatcttcaagaagcgaagagcgatcctctgcatgacgag 485

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Db 61 AAGCAAGAAATGATTTGTTGAGAGGCAAGCAACTGGCATTTTGTGTGATGCTGAG 120
 Qy 466 gtccgcccgcacatcttcccaagaccgcccctctacgaagtacttagcaccagatg 545
 Db 121 GTTGGGTTATGATCTTCTCCAGCATGCAAAACCTATATGATTTCTCCAGCAGCAGCTTG 180
 Qy 546 aatcagctatagatcgtacgcagcccaaggaagagcagcgaagtcgctgccaatccc 605
 Db 181 AGATCAGTAATTTGGTAGTATTAACAAATCAAAAGAGAACATTAATCAACTTGGAGATACA 240
 Qy 606 aactcgagccttaagtttctgcaaaagggagcagcaagccttgagacaacaactcgacaac 665
 Db 241 GCTCTGAAATTAAGTTGGCAAGGAGGAGGAGGAGTGTAAAGCAACAAATTCACAAAT 300
 Qy 666 ttgcaagaagaattatcgcagcttgcagggagatgactcttctggtcgtgaatgtaagaagaa 725
 Db 301 CTGCAGAAATCTCACCGGCAATTAATGGTGAGAGATTAATTCAGGTTTGACAGTCAGAA 360
 Qy 726 ctgcagctccctggagaaatcaatctgaaacaagcctgctgctgctccgcaagaagagac 785
 Db 361 TTACAGGGTTTGGAGAACCAATTTGGAAATTCAGCCTTCTGCTGTGTTCTGATGAAAAGGAG 420
 Qy 786 catctctgataagatgagatcagcagattgaaatcgaaagcaagtliaattaccacaagaa 845
 Db 421 CAACCTTTTATGATGAATACAAAGAACTAAATCGAAAGGGGAGCATCATTTCCACCAAGAA 480
 Qy 846 aatacagactgtacaataagaatcaa 871
 Db 481 AATGTGAACTGTATCTGTAAAGTCTTA 506

RESULT 9

AF312662 916 bp mRNA linear PLN 04-MAY-2001
 LOCUS AF312662
 DEFINITION Arabidopsis thaliana MADS-box protein AGL16 (AGL16) mRNA, partial cds.
 ACCESSION AF312662
 VERSION AF312662.1 GI:11545538
 KEYWORDS

SOURCE

ORGANISM thale cress.
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 916)
 AUTHORS Alvarez-Buylla, E.R., Liljegren, S.J., Pelaz, S., Gold, S.E.,
 Burgel, C., Ditta, G.S., Vergara-Silva, F. and Yanofsky, M.F.
 MADS-box gene evolution beyond flowers: expression in pollen,
 endosperm, guard cells, roots and trichomes
 Plant J. 24 (4), 457-466 (2000)

REFERENCE

TITLE 2 (bases 1 to 916)
 JOURNAL Liljegren, S.J. and Yanofsky, M.F.
 MEDLINE Direct Submission
 20566573
 1115127
 JOURNAL Submitted (12-OCT-2000) Biology, University of California at San
 Diego, 9500 Gilman Drive, La Jolla, CA 92093-0116, USA
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 VSEVBGVKLIANNNSLITNGLDKRDVSNENHVLISOPQHDHETSKAIQINFSTLA"
 BASE COUNT 293 a 193 c 194 g 236 t
 ORIGIN

Query Match 19.5%; Score 249.6; DB 8; Length 916;
 Best Local Similarity 63.2%; Pred. No. 3e-47;
 Matches 384; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

Qy 428 gccccgaagaggatcttcaagaagcgaagggccgcgcacatctctgcatgagcaggt 487
 Db 1 GCGAAGCAATGCAATGTTGTAAGAAAGACTTAAGAGACTTGGCATTTCTCGGATGCTGAGT 60
 Qy 488 cggcctcgtcatcttctccagaccgcccctctacgaagtacttagcaccagatgaa 547
 Db 61 TGGTGTCATCATCTTCTCCAGCACCGGTAGGCTCTACGATTTCTCCAGCTCCAGCATGAA 120
 Qy 548 atcagttatagatcgcgtacgcagcgaagccaaaggaagcagaagtcgtcgcaatcccaa 607
 Db 121 ATCGTCTATGAGAGATACAGCGATGCCAAAGGGGAACCGATTTCAGAAATGATCCGCG 180
 Qy 608 ctccgagccttaagtttctgcaaaagggagcagcagccttgagacaacaactgcacaact 667
 Db 181 TTGCAAAATTCAGTTCTGGSCAAAAGAGGCTCGGATTTCTAAAGCTTCAGCTACATATCTT 240
 Qy 668 gcaagaagaattatcgcagcttgcagggagatgactcttctggtcgtgaatgtaagaagaa 727
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 Db 301 ACAGAAATTTGGAAATCTCAAGCTTAATTTGAGCTTCTGCGGTTGGAATGAAAAAGGATCA 360
 Qy 788 tctctgataagatgagatcagcagattgaaatcgaaagcagatttaccacaagaagaa 847
 Db 361 AATGTTATGGAAGAAATTAACAAGTACTTAACCGAGAGGGAATCTGTTCCACCAAGAGAA 420
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 Qy 908 gatataagagacggaaggaagcagatgagtgatgatactggggagatccgacatcaact 967
 Db 481 GCTTTGAGAGCTGAGGCTGTGAAATTCGCAAAACAAGAAATTCCTTCTGACCAAAAGCTCT 540
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 Db 541 AGACATGAGAGATACCTCGAAGCAACATGTCATCTTCAAGCTGACGCAACCGAGCATGA 600
 Qy 1028 aataaaca 1035
 Db 601 TCATGAGA 608

RESULT 10
 AX085160 310 bp DNA linear PAT 09-MAR-2001
 LOCUS AX085160
 DEFINITION Sequence 10 from Patent WO0112798.
 ACCESSION AX085160
 VERSION AX085160.1 GI:13275252
 KEYWORDS
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 310)
 AUTHORS Loefer, H., Dresselhaus, T., Schreiber, D. and Heuer, S.
 TITLE Male sterile plants
 JOURNAL Patent: WO 0112798-A 10 22-FEB-2001;

Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
 1 (bases 1 to 1039)
 AUTHORS Haung, Y.-S. and Yeh, K.-W.
 TITLE Cloning and characterization of a full-length cDNA encoding a
 MADS-box protein from sweet potato
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1039)
 AUTHORS Haung, Y.-S. and Yeh, K.-W.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUL-2001) Botany, National Taiwan University, No. 1,
 Sec. 4, Roosevelt Rd., Taipei, Taiwan 106, Republic of China
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BASE COUNT 348 a 200 c 238 g 253 t
 ORIGIN

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 Matches 361; Conservative 0; Mismatches 189; Indels 9; Gaps 3;

QY 316 gccaggggtcagaagaagagctagctagctatagcgcggaatcgatggaggaggaaaga 375
 DB 83 GACCAAGCTGCGAAGAACCCCATCCAGAAATAGGAGAGCAAGAGATGGGAGGCGAAGC 142
 QY 376 tgcgtgacgcagagatcgatactaccagcgccgagcgagctgacgttccaaagcgccga 455
 DB 143 TTGAAATTTAGGAGGATGCAAAAGTCGACCAAGCGCAGTACCTTCTTGGAAGAGGAA 202
 QY 436 accggatcttcaagaagcgcaagagctcgccatctctgagatgagcgaggtcgccctg 495
 DB 203 ATGGGTTGTGAAGAGAGCTATGAGATGGGATTTGTGCGATGCTGAAGTGGGATTC 262
 QY 496 tcatctctccagacgcgcgctctacgagtaacttagcacagatgaatcaatga 555
 DB 263 TGATCTTCTCCAGCAGGAGAGCTCCATGATTTGCGAACCTAGCATCAGATCCGTAA 322
 QY 556 tagatcgtagcggaagcgcaaggaaga--gcagcaagctcgtagcaatcccaactcg 612
 DB 323 TTGAACCTTACACACACACAGTGACAGCCTTCAATCCCTCTGAGACCAACATTA 382
 QY 613 agcttaagtttggcaagggagcgcaagcttggagacaacaactgcaacttgcag 672
 DB 383 AACCAAGTTTGGCAATATGAAGTACCAATTCGAGCGCAACAAATTAACACATATCAAG 442
 QY 673 aaatttcgagagttgacgagagatgatacttctgagcggaatgacgaactgca 732
 DB 443 AAGATCATCGGAAGATTAATGGGAGAG--TCTATGCGCTGAGTGTAAAGACTCTCAGA 499
 QY 733 cccttggaatcaatggaacaagcctgctggtgttcgcgcgaagaaggaacatctct 792
 DB 500 ATCTTGAAGCAACGAGGAATGATTTGAGCGGCATGCAATGAGAGAGCAACAATAC 559
 QY 793 tgcataagatgagatcgatgtaatcgaa--aggcaagttatttcaaccaagaata 849
 DB 560 TAATTAACAGATTCAAGAACTAACCCACAGCAGGAGGATTTCGTGACACGAGAAACT 619

QY 850 cagctgtacaataagat 868
 DB 620 TTGAAGCTTTTAATAAGTT 638

RESULT 15
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 DEFINITION Hyacinthus orientalis AgAMOUS homolog transcription factor (HAG1)
 VERSION AF099937
 KEYWORDS
 SOURCE AF099937.2 GI:4887234
 ORGANISM Hyacinthus orientalis.
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
 Hyacinthaceae; Hyacinthus.
 1 (bases 1 to 1061)
 Zhang, X.-S., Li, Q.-Z., and Li, X.-G.
 Regulation of HAG1 expression in the organogenesis system of
 Hyacinthus orientalis in vitro
 Unpublished
 2 (bases 1 to 1061)
 Li, Q.-Z., Zhang, X.-S., and Li, X.-G.
 Direct Submission
 Submitted (19-OCT-1998) College of Life Sciences, Shandong
 Agricultural University, Daizong, Taian, Shandong 271018, P.R.
 China
 3 (bases 1 to 1061)
 Li, Q.-Z., Zhang, X.-S., and Li, X.-G.
 Direct Submission
 Submitted (25-MAY-1999) College of Life Sciences, Shandong
 Agricultural University, Daizong, Taian, Shandong 271018, P.R.
 China
 Sequence update by submitter
 On May 25, 1999 this sequence version replaced gi:4378067.
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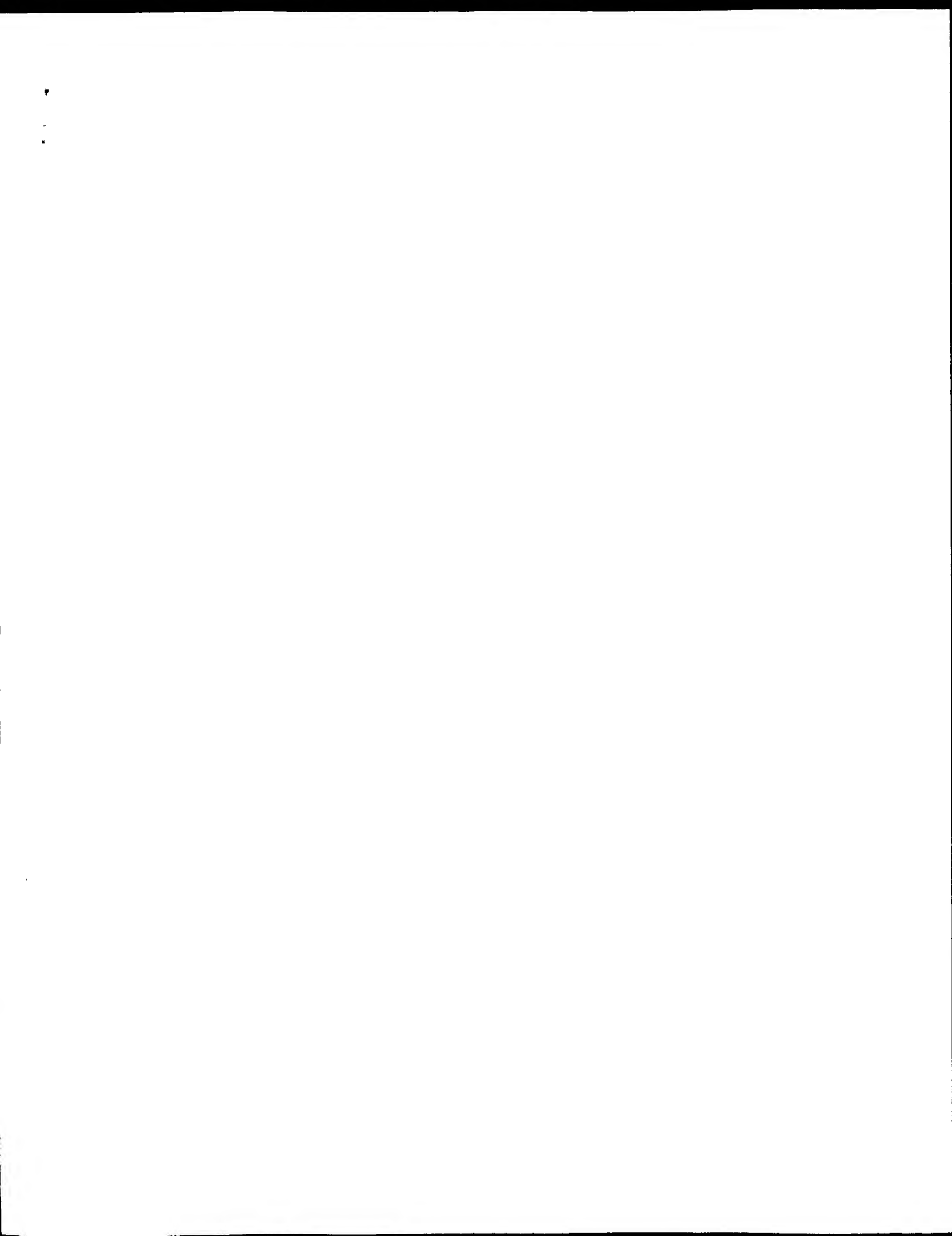
BASE COUNT 326 a 257 c 250 g 228 t
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Query Match 13.8%; Score 176.8; DB 8; Length 1061;
 Best Local Similarity 61.6%; Pred. No. 2.1e-30;
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QY 359 gatgggagggggaagacgctgcatccgagagatgatactccagcgagcgagcgagtg 418
 DB 133 GATGGGAGGGGGAAGATTGAGATTAGCGGATGAGACACCAACGCGGAGGTGAC 192
 QY 419 cttctcaagcgccggaagcgatcttcaagaagcgcaagagctcgcatctcttcgca 478
 DB 193 CTTCTGCAAGCGCGCAACGCGCTTCCTCAAGAGGCGCTACAGAGCTCCGTCCTGCGA 252
 QY 479 tgcgaggttgagctcgatcatcttctccagacacggcgccgctcagagtaactcta--g 535
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Db 253 CGCGAGGTCCGCTTCATCGTCTTCTCCACCCGCGCGCTCTACGAGTACTCCAACTC 312
QY 536 caccagcaltgaatcagttatagatcgtaagcagc---caaggaagagcagcagc 592
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Db 313 CACAGCGCTGAAACGACATTTGAACGATACAGAAAGCTTGCACTGATACACCAACAC 372
QY 593 cgtcgcaaatcccaactcagactlaagtttggcaaaaggagcagcagccttgagaca 652
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Db 373 TGGGACTGTCTGTGAGCTATTTCTCAGTATTTATCAGCAGACAGCAACCAATTACGCA 432
QY 653 acaactgcacaacttgcagaanaattalcgagcttgcagggagatgatcttcttggt 712
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Db 433 GCAATATACCAACTTACAGAACACTTAACAGGACTTTGATGGGAGTCTCTGAGCACCAAT 492
QY 713 gaatgtcaagaactgcagctccctggagaatcaatttgaacaagccttgcgtgtgtc 772
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Db 493 GAGCCTTAGAGACTGAAACAGCTGAGAGGCGAGACTGGAAGAGGCATCAACAAAATPAG 552
QY 773 cgcagaagaagacatctcttgaatagatgcagatttgaatcgaagcagcagttt 832
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Db 553 AACAAAAAGAAAGAGAGCTGTGTCCGCTGAATGCAATACATGCAGAAAAAGGAAAGCGGA 612
QY 833 attcaccagaagaataacagacttgtacaataagat 868
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Db 613 GATGCATATATGATTAACATGTACTTGCGAAATPAGAT 648
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Search completed: August 11, 2002, 08:37:19
Job time: 10179 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 11, 2002, 09:36:03 ; Search time 68.94 Seconds
(without alignments)
602.245 Million cell updates/sec

Title: US-09-970-624-2
1216
Sequence: 1 MGRKIVIRIRIDNSTSHQVT.....PQNNIEPTAPKLGQLIP 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP archaea:*
- 2: SP bacteria:*
- 3: SP fungi:*
- 4: SP human:*
- 5: SP invertebrate:*
- 6: SP mammal:*
- 7: SP mhc:*
- 8: SP organelle:*
- 9: SP phage:*
- 10: SP plant:*
- 11: SP rodent:*
- 12: SP virus:*
- 13: SP vertebrate:*
- 14: SP unclassified:*
- 15: SP virus:*
- 16: SP bacteriophage:*
- 17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1216	100.0	240	09FVN1	Q9FVN1 zea mays (m
2	729.5	60.0	234	P92927	P92927 anilrithium
3	638.5	52.5	234	049351	049351 arabidopsis
4	636.5	52.3	234	09S138	09S138 arabidopsis
5	605	49.8	240	004061	004061 medicago sa
6	597.5	49.1	217	09FEP0	09FEP0 arabidopsis
7	589	48.4	239	09M2M4	09M2M4 arabidopsis
8	544	44.7	218	094ET1	094ET1 ipomoea bat
9	544	36.6	248	041352	041352 silene lat
10	435	35.8	261	040765	040765 picea abies
11	433.5	35.6	238	10 065112	065112 populus tri
12	431.5	35.5	241	10 065111	065111 populus tri
13	428.5	35.2	222	10 040766	040766 picea abies
14	427	35.1	225	10 09SBR3	09SBR3 cucumis sat
15	426.5	35.1	284	10 082732	082732 arabidopsis
16	425.5	35.0	222	10 09ZTV6	09ZTV6 pinus resin

17	425.5	35.0	225	10 043616	043616 petunia hyb
18	425	35.0	261	10 004406	004406 pinus radia
19	424.5	34.9	222	10 09S719	09S719 picea maria
20	424.5	34.9	222	10 09ZRC6	09ZRC6 picea maria
21	424.5	34.9	222	10 09ZTW4	09ZTW4 pinus radia
22	423.5	34.8	228	10 040882	040882 petunia hyb
23	423	34.8	246	10 09S229	09S229 gerbera hyb
24	422.5	34.7	249	10 09SMB3	09SMB3 oryza sativ
25	422	34.7	252	10 09STO6	09STO6 gnetum parv
26	422	34.7	253	10 09XGJ8	09XGJ8 gnetum gnem
27	420	34.5	237	10 09SBR1	09SBR1 cucumis sat
28	420	34.5	262	10 064958	064958 cucumis sat
29	419.5	34.5	228	10 09ZEP9	09ZEP9 hyacinthus
30	419.5	34.5	249	10 09SEV1	09SEV1 oryza sativ
31	416.5	34.3	254	10 09XGJ6	09XGJ6 cucumis sat
32	416	34.2	229	10 064959	064959 gnetum gnem
33	415.5	34.2	246	10 09XFM8	09XFM8 anilrithium
34	415.5	34.2	264	10 09ZS30	09ZS30 gerbera hyb
35	414.5	34.1	221	10 09LKO1	09LKO1 cucumis sat
36	414.5	34.1	284	10 09FEB9	09FEB9 physcomitre
37	414	34.0	258	10 09S3H3	09S3H3 arabidopsis
38	414	34.0	270	10 09SPN2	09SPN2 oryza sativ
39	413	34.0	247	10 09XGK4	09XGK4 gnetum gnem
40	412	33.9	244	10 09XHM3	09XHM3 liquidambar
41	412	33.9	283	10 09FE71	09FE71 physcomitre
42	410	33.7	249	10 09MBE2	09MBE2 rosa rugosa
43	409	33.6	244	10 09ZTV9	09ZTV9 triticum ae
44	408	33.6	242	10 09ZTV9	09ZTV9 corlyus ave
45	407	33.5	254	10 09SBR2	09SBR2 cucumis sat

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	240 AA.
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AC	09FVN1			
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DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	MADS BOX PROTEIN 2.			
GN	MADS2.			
OS	Zea mays (Maize).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;			
OC	Panicoidae; Andropogoneae; Zea.			
OX	NCBI_TaxID=4577;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Al88;			
RA	Heuer S., Loefer H., Dresselhaus T.;			
RT	"The MADS box gene ZmMADS2 is specifically expressed in maize pollen			
RT	and during maize pollen tube growth.";			
RL	Sex. Plant Reprod. 13:21-27(2000).			
DR	EMBL; AF112149; AAG09919.1; -			
DR	HSSP; P11746; 1MN.			
DR	InterPro; IPR002487; K-box.			
DR	InterPro; IPR002100; MADS-box.			
DR	Pfam; PF01486; K-box; 1.			
DR	Pfam; PF00319; SRF-TE; 1.			
DR	PRINTS; PR00404; MADSOMAIN.			
DR	SMART; SM00432; MADS; 1.			
DR	PROSITE; PS00350; MADS_BOX_1; UNKNOWN_1.			
DR	PROSITE; PS00066; MADS_BOX_2; 1.			
SO	SEQUENCE 240 AA; 27415 MW; 5DBP4165CDED984 CRC64;			

Query Match 100.0%; Score 1216; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.6e-76;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 KELOSLENQLETSLSRGVRAKKDHLIDELHDLNRKASLFHOENTDLYNKINLIROENDEL 180
Db 121 KELOSLENQLETSLSRGVRAKKDHLIDELHDLNRKASLFHOENTDLYNKINLIROENDEL 180
QY 181 HKKITETEGSGVNSPPTPFNFVAVETRDVPVQLESTLTPQONNIEPSTAPKGLQILIP 240
Db 181 HKKITETEGSGVNSPPTPFNFVAVETRDVPVQLESTLTPQONNIEPSTAPKGLQILIP 240

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RESULT 2
P92927 PRELIMINARY; PRT; 234 AA.
AC P92927;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE DEFH125 PROTEIN.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97336298; PubMed=9193074;
RT Zaehge S., Seidler H., Schwarz-Sommer Z.;
RT Pollen-specific expression of DEFH125, a MADS-box transcription
RT factor in Antirrhinum with unusual features."
RL Plant J. 11:1043-1050(1997).
DR EMBL; Y10750; CAA71739.1; -.
DR HSSP; P11746; 1NMW.
DR TRANSFAC; T03080; -.
DR InterPro; IPR002487; K-box.
DR InterPro; IPR002100; MADS-box.
DR InterPro; IPR001854; Ribosomal_L29.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRP-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; UNKNOWN_1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
DR SEQUENCE 234 AA; 26882 MW; D69B9216DD4FBE93 CRC64;

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Query Match 60.0%; Score 729.5; DB 10; Length 234;
Best Local Similarity 63.2%; Pred. No. 5.3e-43;
Matches 146; Conservative 32; Mismatches 52; Indels 1; Gaps 1;
QY 1 MGRGKIVIRRIDNSTSRQVTFESKRRNGIFPKKAKELAILCDAEVGLVIFSSGRLYEYST 60
Db 1 MGRGKIVIRRIDNSTSRQVTFESKRRNGIFPKKAKELAILCDAEVGLVIFSSGRLYEYST 60
QY 61 SSKSVIDRYGKAKKEQOVVANNPNSSEKFWQREASLSRQOLHNLQENYQIQRDDLSGLNV 120
Db 61 SSKSVIDRYGKAKKEQOVVANNPNSSEKFWQREASLSRQOLHNLQENYQIQRDDLSGLNV 120
QY 121 KELOSLENQLETSLSRGVRAKKDHLIDELHDLNRKASLFHOENTDLYNKINLIROENDEL 180
Db 121 KELOSLENQLETSLSRGVRAKKDHLIDELHDLNRKASLFHOENTDLYNKINLIROENDEL 180
QY 181 HKKITETEGSGVNSPPTPFNFVAVETRDVPVQLESTLTPQONNIEPSTAPKGLQILIP 240
Db 181 CKKAVYGRDVSANGALVAFGFAIGREPEPIQLHLSQ-PEPENIETSA 230

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RESULT 3

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049351
ID 049351 PRELIMINARY; PRT; 234 AA.
AC 049351;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANR1, MADS-BOX PROTEIN.
GN ANR1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRATIN-LANDSBERG ERECTA (LER);
RX MEDLINE=98092528; PubMed=9430595;
RA Zhang H., Forde B.G.;
RT "An Arabidopsis MADS box gene that controls nutrient-induced changes
RT in root architecture."
RL Science 279:407-409(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; Z97057; CAB09793.1; -.
DR HSSP; P11831; 1SR5.
DR TRANSFAC; T03034; -.
DR InterPro; IPR002487; K-box.
DR InterPro; IPR002100; MADS-box.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRP-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 234 AA; 26805 MW; 721A03A018E25527 CRC64;

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Query Match 52.5%; Score 638.5; DB 10; Length 234;
Best Local Similarity 54.9%; Pred. No. 1e-36;
Matches 135; Conservative 47; Mismatches 43; Indels 21; Gaps 5;
QY 1 MGRGKIVIRRIDNSTSRQVTFESKRRNGIFPKKAKELAILCDAEVGLVIFSSGRLYEYST 60
Db 1 MGRGKIVIRRIDNSTSRQVTFESKRRNGIFPKKAKELAILCDAEVGLVIFSSGRLYEYST 60
QY 60 TSKSVIDRYGKAKKEQOVVANNPNSSEKFWQREASLSRQOLHNLQENYQIQRDDLSGLNV 119
Db 61 SSKSVIDRYGKAKKEQOVVANNPNSSEKFWQREASLSRQOLHNLQENYQIQRDDLSGLNV 120
QY 120 VELOSLENQLETSLSRGVRAKKDHLIDELHDLNRKASLFHOENTDLYNKINLIROENDEL 179
Db 121 ANDLOLEQLETSLSRGVRAKKDHLIDELHDLNRKASLFHOENTDLYNKINLIROENDEL 180
QY 180 LKKITETEGSGVNSPPTPFNFVAVETRDVPVQLESTLTPQONNIEPSTAP 232
Db 181 LKKITETEGSGVNSPPTPFNFVAVETRDVPVQLESTLTPQONNIEPSTAP 232
QY 233 KGLQI 238
Db 228 RGLQI 233

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RESULT 4
Q9S138 PRELIMINARY; PRT; 234 AA.
ID Q9S138;
AC Q9S138;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE MADS-BOX PROTEIN ANR1.
GN AT2G14210.
OS Arabidopsis thaliana (Mouse-ear cress).

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OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:
 OC eurosids II: Brassicales: Brassicaceae: Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RX Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
 DR EMBL: AC007210; AAD25638.1; -;
 DR HSSP: P11831; 1SR5.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription regulation.
 DR KN SEQUENCE 234 AA; 26803 MW; 720F16BC1F72DE27 CRC64;
 SQ
 Query Match 52.3%; Score 636.5; DB 10; Length 234;
 Best Local Similarity 54.9%; Pred. No. 1.4e-36;
 Matches 135; Conservative 46; Mismatches 44; Indels 21; Gaps 5;
 QY 1 MGRGIVIRIDNSTSRQVTFESKRRNGIFKAKELALICDPAVGVIFFSGRLYEY-SS 59
 DB 1 MGRGIVIRIDNSTSRQVTFESKRRSGLIKAKELSLICDPAVGVIFFSGRLYDASN 60
 QY 60 TSMKSVIDRYGKAKEEQVAVNPNSLKFQWEASLRQOLHNLQENYROLTGDDLSGLN 119
 DB 61 TSMKSVIDRYGKAKEEQVAVNPNSLKFQWEASLRQOLHNLQENYROLTGDDLSGLN 120
 QY 120 VKELOSLENQLETSRGVRAKKDHLIDELHDLNKRKASLFHOENTDLYNKINLIQENDE 179
 DB 121 AANDLQLEQVTSKGVYALKYKQDLQMTNRELNRRKQGLQIKQENHNLQIVDIMKRENIK 180
 QY 180 LKKKTY----ETEGPSGVRESPTFENFAVETRVQVLESTL---PQONNIEPTAP 232
 DB 181 LKKKTY----ETEGPSGVRESPTFENFAVETRVQVLESTL---PQONNIEPTAP 232
 QY 233 KLGLOL 238
 DB 238 KLGLOL 238
 DB 228 RGLQOL 233
 RESULT 5
 ID 004061 PRELIMINARY; PRT; 240 AA.
 AC 004061
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MADS-BOX PROTEIN (FRAGMENT).
 OS Medicago sativa (Alfalfa).

OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:
 OC eurosids II: Fabales: Fabaceae: Papilionoideae: Trifoliales: Medicago.
 OX NCBI_TaxID=3879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Dunn K., Heard J.;
 RX Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U91964; AAB51377.1; -;
 DR HSSP: P11746; 1MMN.
 DR TRANSFAC: T03108; -;
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR NON_TER 1
 FT 1
 SQ SEQUENCE 240 AA; 27138 MW; 3E38E21392594D14 CRC64;
 Query Match 49.8%; Score 605; DB 10; Length 240;
 Best Local Similarity 53.6%; Pred. No. 2.1e-34;
 Matches 128; Conservative 32; Mismatches 41; Indels 38; Gaps 4;
 QY 3 RGTIVIRIDNSTSRQVTFESKRRNGIFKAKELALICDPAVGVIFFSGRLYEYSSSM 62
 DB 1 RGTIVIRIDNSTSRQVTFESKRRNGLIKAKELALICDPAVGVIFFSGRLYDASTSL 60
 QY 63 KSVIDRYGKAKEEQVAVNPNSLKFQWEASLRQOLHNLQENYROLTGDDLSGLNKE 122
 DB 61 RSVIGRYNKKKEEKNQGLSTASEIKFCQREAVYLRQOLHNLQESHQIMGEELSLGYKE 120
 QY 123 LQSLLENQLETSRGVRAKKDHLIDELHDLNKRKASLFHOENTDLYNKINLIQENDE 182
 DB 121 LQSLLENQLETSRGVRAKKDHLIDELHDLNKRKASLFHOENTDLYNKINLIQENDE 180
 QY 183 KIVTEGPGGVNR-----ESPFPNFAVETRVQV---OLELSTL 220
 DB 167 KIVTEGPGGVNR-----ESPFPNFAVETRVQV---OLELSTL 222
 RESULT 6
 ID 09PPO PRELIMINARY; PRT; 217 AA.
 AC 09PPO;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MADS-BOX PROTEIN AGL16 (FRAGMENT).
 CN AGL16.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:
 OC eurosids II: Brassicales: Brassicaceae: Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF, STEM, ROOT;
 RX MEDLINE=20566573; PubMed=1115127;
 RA Alvarez-Buylla E.R., Liljegren S.J., Pelaz S., Gold S.E., Burgeff C.,
 RA Ditta G.S., Vergara-Silva F., Yanofsky M.F.;
 RT "MADS-box gene evolution beyond flowers: expression in pollen,
 endosperm, guard cells, roots and trichomes.";
 RL Plant J. 24:457-466(2000).
 DR EMBL: AF312662; AAC37899.1; -;
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.

FT NON_TER 1 1
 SQ SEQUENCE 217 AA; 24853 MW; 8C0E7816396D26BB CRC64;

Query Match 49.1%; Score 597.5; DB 10; Length 217;
 Best Local Similarity 57.8%; Pred. No. 6.1e-34;
 Matches 122; Conservative 38; Mismatches 50; Indels 1; Gaps 1;

QY 24 RRRGIFKKAKELALICDAEVLGFSTGRLEYESTSMKSVTDYRKAKKEQOYVANNP 83
 DB 1 RRRGIFKKAKELALICDAEVLGFSTGRLEYESTSMKSVTDYRKAKKEQOYVANNP 60
 QY 84 SELKFWQREASLRQOLHNIDENYRQLTGDDSLGNKELQSLQENOLETSLRGVRAKKDH 143
 DB 61 SEIOFWQREASLRQOLHNIDENYRQLTGDDSLGNKELQSLQENOLETSLRGVRAKKDH 120
 QY 144 LLIDEIDHNRKASLFEQENTDLYNKINILROENDELHKIYETEGSGVNRSPPTPFNF 203
 DB 121 MLIEIOLVNRKASLFEQENTDLYNKINILROENDELHKIYETEGSGVNRSPPTPFNF 180
 QY 204 AVETRDVYQLESLTPQONNIEPTAPKL 234
 DB 181 DMRTSNEHVHLQSLQ-PQDHETHSKAIQL 210

RESULT 7
 Q9M2M4 PRELIMINARY; PRT; 239 AA.

AC Q9M2M4;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE MADS-BOX TRANSCRIPTION FACTOR-LIKE PROTEIN.
 GN F2809.80.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Benes V., Rechmann S., Borkova D., Ansojge W., Mewes H.W., Lemcke K.,
 Mayer K.F.X., Quetier F., Salanoubat M.,
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Arabidopsis sequencing project;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL137080; CAB68129.1;
 DR HSSP; P11746; 1MNM.
 DR InterPro; IPR002487; K-box.
 DR InterPro; IPR002100; MADS-box.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PRO0404; MADSOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00035; MADS_BOX_1; UNKNOWN_1.
 DR PROSITE; PS00066; MADS_BOX_2; 1.
 SQ SEQUENCE 239 AA; 27233 MW; CEA20AC4F98D45DB CRC64;

Query Match 48.4%; Score 589; DB 10; Length 239;
 Best Local Similarity 53.3%; Pred. No. 2.6e-33;
 Matches 130; Conservative 39; Mismatches 53; Indels 22; Gaps 4;

QY 1 MGRGKIVIRINDNSTSQVTFKRRNGIFKKAKELALICDAEVLGFSTGRLEYEST 60
 DB 1 MGRGKIVIRINDNSTSQVTFKRRNGIFKKAKELALICDAEVLGFSTGRLEYEST 60
 QY 61 SKMSVTDYRKAKKEQOYVANNPSELKFWQREASLRQOLHNIDENYRQLTGDDSLGN 110
 DB 61 SKMSVTDYRKAKKEQOYVANNPSELKFWQREASLRQOLHNIDENYRQLTGDDSLGN 109

QY 111 TGGDLSGLNWEKQSLQENOLETSLRGVRAKKDHLLIDEIDHNRKASLFEQENTDLYNKI 170
 DB 110 MGEISGLSVKALQENOLETSLRGVRAKKDHLLIDEIDHNRKASLFEQENTDLYNKI 169
 QY 171 NLIROENDELHKIYETEGSGVNRSPPTPFNFVETRDVYQLESLTPQONNIEPT 230
 DB 170 NLIROENDELHKIYETEGSGVNRSPPTPFNFVETRDVYQLESLTPQONNIEPT 228
 QY 231 AKRL 234
 DB 229 AIQL 232

RESULT 8
 Q94ET1 PRELIMINARY; PRT; 218 AA.

AC Q94ET1;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE MADS-BOX PROTEIN.
 GN MADS1.
 OS Ipomoea batatas (Sweet potato) (Batale).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
 OX NCBI_TaxID=4120;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haung Y.-S., Yeh K.-W.,
 RT "Cloning and characterization of a full-length cDNA encoding a MADS-
 box protein from sweet potato."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF396746; AAK83920.1;
 SQ SEQUENCE 218 AA; 25222 MW; 788D47FEB8D02DC8 CRC64;

Query Match 44.7%; Score 544; DB 10; Length 218;
 Best Local Similarity 50.0%; Pred. No. 3e-30;
 Matches 112; Conservative 46; Mismatches 48; Indels 18; Gaps 5;

QY 1 MGRGKIVIRINDNSTSQVTFKRRNGIFKKAKELALICDAEVLGFSTGRLEYEST 60
 DB 1 MGRGKIVIRINDNSTSQVTFKRRNGIFKKAKELALICDAEVLGFSTGRLEYEST 60
 QY 61 SKMSVTDYRKAKKEQOYVANNPSELKFWQREASLRQOLHNIDENYRQLTGDDSLGN 119
 DB 61 SIRVTEIKNTQGDLSQSLDPTLLEKFWQREASLRQOLHNIDENYRQLTGDDSLGN 119
 QY 120 VKEQSLQENOLETSLRGVRAKKDHLLIDEIDHNRKASLFEQENTDLYNKINILROEND 178
 DB 120 VKDQSLQENOLETSLRGVRAKKDHLLIDEIDHNRKASLFEQENTDLYNKINILROEND 171
 QY 179 ELHKIYETEGSGVNRSPPTPFNFVETRDVYQLESLTPQONNIEPT 222
 DB 172 ---QAVGTSQNAVNAGPTISPYDFTISESQGHIFQ---LPQ 208

RESULT 9
 Q41352 PRELIMINARY; PRT; 248 AA.

AC Q41352;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE SIM1 PROTEIN.
 GN SIM1.
 OS Silene latifolia.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=37657;
 RN [1]


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Db      16 LGKGVKLEIKRIENTNROVYTFCKRRNGILKKAKYELSVLCDAEVALIVFSSRGRLYESNN 75
      61 SMKSVIDRYGKA---KEEOYVAMPNSLKFWRPAAASLRQOLHNLQENYRQLTGDDLSG 117
      76 SVKSTIERKRYKACADSSNNGSVSEANAQ--FYQOEAKLRSQIGNLQNSNMMLGSELSA 133
Qy      118 LNVKELOSLLENOLETSLRGVRAKKDHLLIDETIDLNRKASLFHOENLDYKIMLR-- 174
      134 LSVKELKSLKLEIKRIGRISKRNELLFAEIEYMKR-----EIDLHNNOLLRAKI 186
Qy      175 QENDELHKKIYEIEGPGSVNRE--SPFPEN 202
      187 AENE--RRQHMNLMPGCVNFEIMOSOPD 214

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RESULT 12
ID      065111      PRELIMINARY;      PRT;      241 AA.
AC      065111;
DT      01-AUG-1998 (TREMBlrel. 07, Created)
DT      01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT      01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE      AGAMOUS HOMOLOG.
GN      Populus trichocarpa (Western balsam poplar).
OS      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids I; Malpighiales; Salicaceae; Populus.
OX      NCBI_TaxID=3694;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Brunner A.M., Rottmann W.H., Sheppard L.A., Strauss S.H.;
RT      "Two Populus trichocarpa genes homologous to AGAMOUS.";
RT      Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC      -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC      -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR      EMBL; AF052570; AAC06237.1;
DR      HSSP; P11746; 1MNM.
DR      InterPro; IPR002487; K-box.
DR      InterPro; IPR002100; MADS-box.
DR      Pfam; PF01486; K-box; 1.
DR      Pfam; PF00319; SRF-TF; 1.
DR      PRINTS; PR00404; MADSOMAIN.
DR      SMART; SM00432; MADS; 1.
DR      PROSITE; PS00350; MADS_BOX_1; 1.
DR      PROSITE; PS50066; MADS_BOX_2; 1.
KW      DNA-binding; Nuclear protein; Transcription regulation.
SQ      SEQUENCE 241 AA; 27559 MW; 4C2BFD11F29E99CF CRC64;

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Query Match 35.5%; Score 431.5; DB 10; Length 241;
 Best Local Similarity 40.0%; Pred. No. 1.9e-22;
 Matches 100; Conservative 52; Mismatches 63; Indels 35; Gaps 7;

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Qy      1 MGRGKIVIRIDNSTSRVTFSKRRNGIFKKAKELAILCDAEGLVIFSTGRLEYEST 60
      16 LGKGVKLEIKRIENTNROVYTFCKRRNGILKKAKYELSVLCDAEVALIVFSSRGRLYESND 75
Qy      61 SMKSVIDRYGKAKEEOO---VANPNSLKFWRPAAASLRQOLHNLQENYRQLTGDDLSG 117
      76 SVKSTIERKRYKACADSSNNGSVSEANAQ--FYQOEAKLRSQIGNLQNSNMMLGSELSA 133
Qy      118 LNVKELOSLLENOLETSLRGVRAKKDHLLIDETIDLNRKASLFHOENLDYKIMLR-- 177
      134 LSVKELKSLKLEIKRIGRISKRNELLFAEIEYMKR-----EVDLHNNOLLRAKI 186
Qy      178 DELHKKIYEIEGPGSVNRES---PTFPNPAVETRDVQULETLDPQNNIEP-----S 229
      187 SEHERR-----RQSMNLMPGCAPEIYOSO-----PIDSRYNSOYVNGLOPASHYS 231
Qy      230 TAPKLGLOLI 239
      : : : : :

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Db 232 HODOMALQIV 241

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RESULT 13
ID      040766      PRELIMINARY;      PRT;      222 AA.
AC      040766;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE      DAL2 PROTEIN.
GN      Picea abies (Norway spruce) (Picea excelsa).
OS      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX      NCBI_TaxID=3329;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      TISSUE=FEMALE CONE;
RA      MEDLINE=95170009; PubMed=7865797;
RA      Tandere K., Albert V.A., Sundas A., Engstrom P.;
RT      "Conifer homologues to genes that control floral development in
RT      angiosperms.";
RL      Plant Mol. Biol. 27:69-78(1995).
CC      -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC      -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR      EMBL; X79280; CAA55867.1;
DR      HSSP; P11746; 1MNM.
DR      TRANSFAC; T03076; -.
DR      InterPro; IPR002487; K-box.
DR      InterPro; IPR002100; MADS-box.
DR      Pfam; PF01486; K-box; 1.
DR      Pfam; PF00319; SRF-TF; 1.
DR      PRINTS; PR00404; MADSOMAIN.
DR      SMART; SM00432; MADS; 1.
DR      PROSITE; PS00350; MADS_BOX_1; 1.
DR      PROSITE; PS50066; MADS_BOX_2; 1.
KW      DNA-binding; Nuclear protein; Transcription regulation.
SQ      SEQUENCE 222 AA; 25638 MW; 5369D7B62B8E77D9 CRC64;

```

Query Match 35.2%; Score 428.5; DB 10; Length 222;
 Best Local Similarity 50.9%; Pred. No. 2.8e-22;
 Matches 88; Conservative 35; Mismatches 45; Indels 5; Gaps 2;

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Qy      1 MGRGKIVIRIDNSTSRVTFSKRRNGIFKKAKELAILCDAEGLVIFSTGRLEYEST 60
      16 LGKGVKLEIKRIENTNROVYTFCKRRNGILKKAKYELSVLCDAEVALIVFSSRGRLYERANH 60
Qy      61 SMKSVIDRYGKAKEEOO---VANPNSLKFWRPAAASLRQOLHNLQENYRQLTGDDLSG 117
      61 SVKSTIERKRYKACADSSNNGSVSEANSO--YWOEAGKLRQOILHNLHNMMLGDDGTLA 118
Qy      118 LNVKELOSLLENOLETSLRGVRAKKDHLLIDETIDLNRKASLFHOENLDYKIMLR-- 170
      119 LNIKRLKOLEVRLKLGIRVSKKNEMLEIDIMQREHILIOENELTAKI 171
Qy      178 DELHKKIYEIEGPGSVNRES---PTFPNPAVETRDVQULETLDPQNNIEP-----S 229
      187 SEHERR-----RQSMNLMPGCAPEIYOSO-----PIDSRYNSOYVNGLOPASHYS 231
Qy      230 TAPKLGLOLI 239
      : : : : :

```


7
:
:

Claim 1; Page 66-67; 76pp; English.

The present invention provides the protein and coding sequences of the Zea mays ZmMADS2 protein, which is specifically expressed in pollen. The sequences can be used to produce male sterile plants, as ZmMADS2 is essential for pollen tube growth. These are useful in hybrid breeding, particularly of corn, cereal and grain. The present sequence is the ZmMADS2 protein.

Sequence 240 AA;

Query Match 100.0%; Score 1216; DB 22; Length 240;
Best Local Similarity 100.0%; Pred. No. 3.5e-102;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRGKIVIRRIDNSTSRQVTFKRRNGIFPKAKELAILCDAEVLGFSTGRLEYSSST 60
DB 1 mgrgkivirridnstsrqvtfskrrngifkkaelailcdaevglvifstgrleyssst 60
QY 61 SMKSVIDRYGKAKEEQVAVNPNSSELKFWQREASLRQQLHNLQENYRQLTGDDLSGLNV 120
DB 61 smksvidrygkakeeqvavnpnpselkfwgreaaslrqqlhnlqenyrgltgddlsglnv 120
QY 121 KELQSLNQLTSLRGVRAKDKHLLIDEIHDNLNRKASLFHQENTDLYNKINLRQENDEL 180
DB 121 kelqslengletslrgvrakdkhllideihdlnrkaslfhgentdlynkinlrqendel 180
QY 181 HKKIYETEGPSGVNRESPTPFNFVAVVTRDVPVQLSTLPQNNIEPSTAPKLGILQLIP 240
DB 181 hkkiiyetegpsgvnresptpfnfavvtrdvpvqlstlpqnniepstapklgqlip 240

RESULT 2

AAB73333
ID AAB73333 standard; Protein; 1240 AA.

AC AAB73333;

DT 22-MAY-2001 (first entry)

DE Maize ZmMADS2 protein, SEQ ID NO:2.

KW Maize MADS box gene; ZmMADS2; pollen-specific expression;
KW pollen development; function; transgenic plant; male sterility;
KW hybrid seed production.

OS Zea mays.

PN WO200112799-A2.

PD 22-FEB-2001.

PF 16-AUG-2000; 2000WO-EP08002.

PR 18-AUG-1999; 99EP-0116268.

PA (SUED-) SUEDEWSTDEUTSCHE SAATZUCHT.

PI Loerz H, Dresselhaus T, Schreiber D, Heuer S;

XX WPI; 2001-211214/21.

DR N-PSDB; AAF76058, AAF76068;

XX Novel nucleic acid molecule useful for cloning and expressing a pollen
PT specific sequence in a plant

XX Example 1; Page 56-57; 66pp; English.

CC The invention relates to regulatory elements (AAF76059-AAF76067) from
CC the maize MADS box gene ZmMADS2 (AAF76068) which are capable of directing
CC expression in a pollen-specific manner. The ZmMADS2 protein (AAB73333)
CC is expressed particularly in mature pollen after dehiscence, indicating

CC that it has an essential role in pollen development and function, in
CC particular in pollen tube growth. The invention also relates to vectors
CC and host cells comprising the ZmMADS2 regulatory or genomic sequence, and
CC their use in the generation of transgenic plants. The ZmMADS2 regulatory
CC sequences are useful for cloning and expressing a pollen-specific or
CC pollen-abundant gene in a plant, and may also be used to drive the
CC expression of a gene of interest in a pollen-specific or pollen-preferred
CC manner. The ZmMADS2 regulatory sequences are useful for isolating related
CC regulatory sequences of other plant species which confer pollen or group
CC specificity to genes of interest operably linked to them. The regulatory
CC sequences are useful in plant breeding, especially for the production of
CC hybrid seed. In particular, they may be used to drive the pollen-specific
CC expression of heterologous genes which confer nuclear or cytoplasmic male
CC sterility in transgenic plants (e.g., cereals). The present sequence
CC represents ZmMADS2 protein.

XX SQ Sequence 240 AA;

Query Match 100.0%; Score 1216; DB 22; Length 240;
Best Local Similarity 100.0%; Pred. No. 3.5e-102;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRGKIVIRRIDNSTSRQVTFKRRNGIFPKAKELAILCDAEVLGFSTGRLEYSSST 60
DB 1 mgrgkivirridnstsrqvtfskrrngifkkaelailcdaevglvifstgrleyssst 60
QY 61 SMKSVIDRYGKAKEEQVAVNPNSSELKFWQREASLRQQLHNLQENYRQLTGDDLSGLNV 120
DB 61 smksvidrygkakeeqvavnpnpselkfwgreaaslrqqlhnlqenyrgltgddlsglnv 120
QY 121 KELQSLNQLTSLRGVRAKDKHLLIDEIHDNLNRKASLFHQENTDLYNKINLRQENDEL 180
DB 121 kelqslengletslrgvrakdkhllideihdlnrkaslfhgentdlynkinlrqendel 180
QY 181 HKKIYETEGPSGVNRESPTPFNFVAVVTRDVPVQLSTLPQNNIEPSTAPKLGILQLIP 240
DB 181 hkkiiyetegpsgvnresptpfnfavvtrdvpvqlstlpqnniepstapklgqlip 240

RESULT 3

AAG31142
ID AAG31142 standard; Protein; 228 AA.

AC AAG31142;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 37350.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2002, 08:37:25 ; Search time 61.65 Seconds

(without alignments)

432.404 Million cell updates/sec

Title: US-09-970-624-2

Perfect score: 1216

Sequence: 1 MGRKIVIRIDNSTSRQVT.....PQNNIRPSTAPKLGQLIP 240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1216	100.0	240	22	Maize ZmMADS2 SEQ
2	1216	100.0	240	22	Maize ZmMADS2 prot
3	666	54.8	228	21	Arabidopsis thalia
4	643.5	52.9	227	21	Arabidopsis thalia
5	636.5	52.3	234	21	Arabidopsis thalia
6	633.5	52.1	238	21	Arabidopsis thalia
7	433.5	35.6	238	21	Poplar PTAG-2 flori
8	433.5	35.6	238	21	Poplar PTAG-2 flori
9	431.5	35.5	241	21	Amino acid sequenc
10	431.5	35.5	241	21	Poplar PTAG-1 flori
11	431	35.4	185	21	Amino acid sequenc
					Eucalyptus grandis

12	431	35.4	229	17	AA999637	Eucalyptus AGE-2 p
13	426.5	35.1	300	21	AA952721	Arabidopsis thalia
14	425	35.0	261	19	AAW48623	Pinus radiata cone
15	424.5	34.9	222	21	AAW26795	Plant reproductive
16	420	34.5	221	21	AAW44804	Petunia hybrida ne
17	420	34.5	221	21	AAW58648	Petunia nectary-sp
18	419.5	34.5	230	21	AAW16690	Arabidopsis thalia
19	419.5	34.5	230	21	AAW40213	Arabidopsis thalia
20	419.5	34.5	277	21	AAW16689	Arabidopsis thalia
21	419.5	34.5	277	21	AAW40212	Arabidopsis thalia
22	417	34.3	246	20	AAW81000	Arabidopsis AGU5 p
23	414	34.0	251	21	AAW34121	Zea mays protein f
24	414	34.0	258	21	AAW32583	Arabidopsis thalia
25	414	34.0	307	21	AAW34120	Zea mays protein f
26	412.5	33.9	262	21	AAW69920	MADS box protein.
27	407	33.5	167	21	AAW31143	Arabidopsis thalia
28	406	33.4	268	21	AAW43856	Zea mays protein f
29	405	33.3	248	20	AAW80999	Arabidopsis AGU1 p
30	405	33.3	248	21	AAW09411	Arabidopsis thalia
31	402.5	33.1	242	19	AAW48622	Pinus radiata cone
32	402	33.1	257	21	AAW33135	Zea mays protein f
33	402	33.1	260	21	AAW33134	Zea mays protein f
34	402	33.1	283	21	AAW33133	Zea mays protein f
35	401	33.0	248	20	AAW84050	Rice OSMADS8 prote
36	401	33.0	251	17	AAW99633	Eucalyptus AGE-1 p
37	401	33.0	257	17	AAW99631	OSMADS1 protein.
38	398	32.7	181	21	AAW33310	Pinus radiata tran
39	396.5	32.6	161	21	AAW33229	Eucalyptus grandis
40	395.5	32.5	240	21	AAW96767	Z. mays MADS-box p
41	393	32.3	253	19	AAW69329	Brassica oleracea
42	393	32.3	253	19	AAW43110	APETAL1 gene prod
43	393	32.3	253	19	AAW39132	Brassica floral me
44	393	32.3	253	19	AAW43327	Brassica floral me
45	393	32.3	253	21	AAW19242	Amino acid sequenc

ALIGNMENTS

RESULT 1

AAW72888

ID AAW72888 standard; Protein; 240 AA.

XX

AC AAW72888;

XX

DT 11-MAY-2001 (first entry)

XX

DE Maize ZmMADS2 SEQ ID NO: 2.

XX

KW Male sterile plant; maize; hybrid breeding; pollen tube; ZmMADS2;

KW grain; cereal; corn.

XX

OS Zea mays.

XX

PN WO200112798-A2.

XX

PD 22-FEB-2001.

XX

PF 16-AUG-2000; 2000WO-EP08001.

XX

PR 18-AUG-1999; 99EP-0116267.

XX

(SUED-) SUEDEWESTDEUTSCHE SAATZUCHT.

XX

PI Loerz H, Dresselhaus T, Schreiber D, Heuer S;

XX

DR WPI; 2001-211213/21.

XX

PT Novel nucleic acid molecule, ZmMADS2 derived from pollen of Zea mays

PT useful for cloning and expressing a pollen specific sequence in a plant

PT and for producing male sterile plants

XX

PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
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Query Match 52.1%; Score 633.5; DB 21; Length 238;
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 AC AAY58657;

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XX 11-APR-2000 (first entry)
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XX Poplar PTAG-2 floral homeotic gene-encoded protein.
DE
XX Poplar; PTAG-2: floral homeotic gene; transgenic plant; sterility;
KW fertility.
XX Populus balsamifera subsp. trichocarpa.
OS
XX
XX Key Location/Qualifiers
FH Domain 17..33
FT /note="MADS domain"
FT 106..172
FT Domain /note="K domain"
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XX 07-APR-1998: 98CA-2227940.
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XX 06-APR-1998: 98US-0080851.
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XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Rottmann WH, Brunner AM, Sheppard LA, Strauss SH,
XX
XX WPI: 2000-106662/10.
XX N-PSDB: AAZ57848, AAZ57949.
XX
XX Nucleic acid from Populus trichocarpa genes, useful for producing
PT transgenic plants, particularly trees, with modified fertility
PT characteristics such as sterility.
XX
XX Claim 31: Page 77; 92pp: English.
XX
XX The present sequence is that of the novel PTAG-2 protein of poplar
XX (Populus balsamifera subsp. trichocarpa), as deduced from newly
XX isolated gene and cDNA sequences (see AAZ57948-49). PTAG-2 is 1
XX of 4 novel floral homeotic genes identified in this poplar species.
XX It is a homologue of AGAMOUS and is expressed in floral tissues.
XX CC PTAG-2 contains a MADS domain and a K-domain. The invention
XX provides nucleic acid sequences of the 4 novel Populus genes, the
XX corresponding cDNA sequences (see AAZ47942-49) and deduced amino acid
XX sequences (see AAY58454-57). It also provides methods of using the
XX gene and cDNA sequences to produce genetically engineered Populus
XX and other trees having modified fertility characteristics, including
XX sterility. Genetic constructs useful in producing genetically
XX engineered Populus and other trees include antisense versions of
XX CC PTAG-2, dominant negative mutants, and constructs useful for sense
XX suppression. Sterile trees allow increased wood yield and a
XX reduction in the production of allergens such as pollen.
XX
XX Sequence 238 AA:
SQ
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KW LFY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
KW fertility; sterility.
XX
XX Populus balsamifera.
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XX Key Location/Qualifiers
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XX 01-APR-2001.
XX
XX 02-OCT-2000; 2000CA-2319853.
XX
XX 01-OCT-1999; 99US-0410464.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Rottman WH, Strauss SH, Brunner AM, Sheppard LA;
XX
XX WPI: 2001-336098/36.
XX N-PSDB: AAF85400, AAF85401, AAF85402.
XX
XX Novel isolated polynucleotide derived from Populus species, useful for
PT producing transgenic plants having modified fertility characteristic,
PT particularly sterility.
XX
XX Claim 23: Page 62-63; 69pp: English.
XX
XX The present sequence represents a floral homeotic protein, designated
XX PTAG-2, which is derived from Populus balsamifera subsp. trichocarpa.
XX The specification also describes PTD, PTLF, and PTAG-1 proteins. The
XX CC floral homeotic proteins are expressed in floral tissues. PTLF is a
XX CC homologue of LEAFY (LFY) and FLORICAULA (FLO), and is expressed in
XX CC immature inflorescences on which floral primordia are developing. PTD
XX CC is a homologue of DEFICIENS (DEF), and is strongly expressed in stamen
XX CC primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are
XX CC homologues of AGAMOUS (AG). The floral homeotic proteins and
XX CC polynucleotides are useful for producing transgenic plants having
XX modified fertility characteristics, particularly sterility.
XX
XX Sequence 238 AA:
SQ
Query Match 35.6%; Score 433.5; DB 22; Length 238;
Best Local Similarity 46.7%; Pred. No. 2,9e-31;
Matches 98; Conservative 39; Mismatches 54; Indels 19; Gaps 6;
QY 1 MGKGIYIRIDNSTSQVFFSKRRNGIFKKAKELATICDAEGLVIFSTGRLEYST 60
DB 16 Igrkvvelkrlentunrgvtfckrrngllkkayelsvdcdaevalivfsrgriyeynn 75
QY 61 SMKSVIDRYGKA---KEEQOVVANNPNSLKWQREAAASLRQOLHNIOENYRLTGDDLSG 117
DB 134 lsvkelstlelklekgigrlfrrskkneillfaeleymqr-----eidlhnmgllraki 186

```

Db 76 svkstlerykkacadsnnsgvseanaq--fygqaekalrsglgnlqnsnrmlgesls 133
 QY 118 LNVKELOSLENOLETSLRGVRAKKDHLIDETIDLNKRAKSLFHQENTDLYNKINILR-- 174
 Db 134 lsvkelksleirlekygrilrskkneillfaeleymqkr-----edlhnngqlllrakl 186
 QY 175 QENDELHKRIYETEGSPGVNRE--SPTEPN 202
 Db 187 aene--rkrqhmhmpgyvfeimsgpdl 214

RESULT 9

AAV58656

ID AAV58656 standard; Protein; 241 AA.

AC AAV58656;

DT 11-APR-2000 (first entry)

DE Poplar PRAG-1 floral homeotic gene-encoded protein.

KW Poplar; PRAG-1; floral homeotic gene; transgenic plant; sterility;
 XX fertility.

OS Populus balsamifera subsp. trichocarpa.

FH Key Location/Qualifiers

FT Domain 17..33 /note= "MADS domain"

FT Domain 106..172 /note= "K domain"

CA2227940-A1.

06-OCT-1999.

07-APR-1998; 98CA-2227940.

06-APR-1998; 98US-0080851.

(UYOR-) UNIV OREGON HEALTH SCI.

Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;

WPI: 2000-106662/10.

N-PSDB; AAZ57946, AAZ57947.

XX Nucleic acid from Populus trichocarpa genes, useful for producing
 PT transgenic plants, particularly trees, with modified fertility
 PT characteristics such as sterility -

Claim 31; Page 67-68; 92pp; English.

XX The present sequence is that of the novel PRAG-1 protein of poplar
 CC (Populus balsamifera subsp. trichocarpa), as deduced from newly
 CC isolated gene and cDNA sequences (see AAZ57946-47). PRAG-1 is 1
 CC of 4 novel floral homeotic genes identified in this poplar species.
 CC It is a homologue of AGAMOUS and is expressed in floral tissues.
 CC PRAG-1 contains a MADS domain and a K-domain. The invention
 CC provides nucleic acid sequences of the 4 novel Populus genes, the
 CC corresponding cDNA sequences (see AAZ47942-49) and deduced amino acid
 CC sequences (see AAV58454-57). It also provides methods of using the
 CC gene and cDNA sequences to produce genetically engineered Populus
 CC and other trees having modified fertility characteristics, including
 CC sterility. Genetic constructs useful in producing genetically
 CC engineered Populus and other trees include antisense versions of
 CC PRAG-1, dominant negative mutants, and constructs useful for sense
 CC suppression. Sterile trees allow increased wood yield and a
 CC reduction in the production of allergens such as pollen.

Sequence 241 AA;

Query Match 35.5%; Score 431.5; DB 21; Length 241;
 Best Local Similarity 40.0%; Pred. No. 4,4e-31;
 Matches 100; Conservative 52; Mismatches 63; Indels 35; Gaps 7;

QY 1 MGRKIVIRRDNDSRQVFEKRRNGIEKKAKELALICDAEGLVIFSTGRLYESSST 60
 Db 16 lgrgkveikritentunqvlckrrsgllkayelsvldaeavallvfsrgrlyesnd 75
 QY 61 SMKSVIDRYKAKEEQD--VVANPNSLEKFWQREASLRQOLHNQENRQLTGDLG 117
 Db 76 svkstlerykkacadsnnsgvseanaq--yfgqaekalrsglgnlqnsnrmlgesals 133
 QY 118 LNVKELOSLENOLETSLRGVRAKKDHLIDETIDLNKRAKSLFHQENTDLYNKINILRQEN 177
 Db 134 lsvkelksleirlekygrilrskkneillfaeleymqkr-----evdlhnngqlllrakl 186
 QY 178 DELHKRIYETEGSPGVNRES--PTPEFNNAVYETDVPQLESLRPGQNNIEP-----S 229
 Db 187 seneik-----rsgmlmpgadtelvsgq-----pydsrnysgvnglqpsahys 231
 QY 230 TAPKLGLOLI 239
 Db 232 hgdqmalqlv 241

RESULT 10

ID AAB68437 standard; Protein; 241 AA.

AAB68437;

23-JUL-2001 (first entry)

DE Amino acid sequence of the floral homeotic protein PRAG-1.

KW Floral homeotic gene; PTD; PTLF; PRAG-1; PRAG-2; floral tissue; LEAFY;
 KW LEF; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
 XX fertility; sterility.

OS Populus balsamifera.

FH Key Location/Qualifiers

FT Domain 17..72 /note= "MADS domain"

FT Domain 106..172 /note= "K domain"

CA2319853-A1.

01-APR-2001.

02-OCT-2000; 2000CA-2319853.

01-OCT-1999; 99US-0410464.

(UYOR-) UNIV OREGON HEALTH SCI.

Rottman WH, Strauss SH, Brunner AM, Sheppard LA;

WPI: 2001-336098/36.

N-PSDB; AAF85397, AAF85398, AAF85399.

XX Novel isolated polynucleotide derived from Populus species, useful for
 PT producing transgenic plants having modified fertility characteristic,
 PT particularly sterility -

Claim 23; Page 56-57; 69pp; English.

XX The present sequence represents a floral homeotic protein, designated
 CC PRAG-1, which is derived from Populus balsamifera subsp. trichocarpa.
 CC The specification also describes PTD, PTLF, and PRAG-2 proteins. The
 CC floral homeotic proteins are expressed in floral tissues. PTLF is a
 CC homologue of LEAFY (LFY) and FLORICAULA (FLO), and is expressed in

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JUN 10 1964
U.S. DEPARTMENT OF AGRICULTURE
WASHINGTON, D.C.

PR	23-APR-1999;	9905-01305011
PR	23-APR-1999;	9905-01308911
PR	28-APR-1999;	9905-0131449
PR	30-APR-1999;	9905-01320408
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[illegible]

XX (EBIN-) FB INVESTMENTS PTY LTD.
 XX Teasdale RD;
 XX WPI: 1998-230712/20.
 XX N-PSDB: AAV18014.
 XX
 XX Method of enhancing vegetative growth in plant - comprises use of
 XX expression cassette containing heterologous coding region expressing
 XX product which aborts development
 XX
 XX Disclosure; Fig 14; 96pp; English.
 XX
 XX This is the amino acid sequence of the PRMADS3 protein of Pinus
 XX radiata, deduced from an isolated cDNA clone (see AAV18012).
 XX Expression of PRMADS3 is restricted to male and female cones. The
 XX PRMADS1, 2 and 3 proteins (see also AAV48622 and AAV48623) have been
 XX expressed in E. coli and characterised as DNA binding proteins.
 XX Their DNA binding consensus sequence is similar to that of the
 XX AGAMOUS protein. All 3 proteins bind a DNA sequence matching the
 XX consensus sequence of the CARG box. The invention relates to genes
 XX from reproductive tissues of Pinus radiata and Eucalyptus grandis
 XX and the use of the promoters (see AAV18013, AAV18015, AAV18017 and
 XX AAV18019-22) of such genes in expression cassettes used to modify a
 XX plant, especially a tree used in timber, pulp or fibre production,
 XX to increase vegetative growth and thus production of valuable
 XX material.
 XX
 XX Sequence 261 AA;
 XX

Query Match 35.0%; Score 425; DB 19; Length 261;
 Best Local Similarity 40.8%; Pred. No. 1.9e-30;
 Matches 89; Conservative 44; Mismatches 61; Indels 24; Gaps 4;
 QY 1 MGRKIVIRINDNSTQVTFKRRNGIFKAKELALICDAEVLGVTSSTGRLEYEST 60
 DB 1 mgrkviririndnstqvtfkrrngifkakealalicaeavlgsstgrleyest 60
 QY 61 SMKSVIRRYGKAK-EEQOVVANPNSLSEKFWOREAASLRQOLHNLQENYRQLTGDDLSGLN 119
 DB 61 smksvirrygkaks-eeqovvanpnslsekfworeaslrqolhnlqenyrltgddls 119
 QY 120 VKEIQLSLENQLETSLRGVRRAKDHLLIDETIHDLNRKASLFRHOENTDLYNKINIRQENDE 179
 DB 120 vkeiqqlslenqletsrgvrrakdhllidetihdlnrkaslfrhoentdlynkinir 179
 QY 180 LHKRIYEEGP---SGVNRSEPT-----PENFAVET 208
 DB 167 lqkriyeegep---sgvnrsept-----penfavet 204

RESULT 15
 AAB26795
 ID AAB26795 standard; Protein; 222 AA.
 XX
 XX AAB26795;
 XX
 XX 22-JAN-2001 (first entry)
 XX
 XX Plant reproductive tissue promoter protein.
 XX
 XX Plant promoter; PRAG1; reproductive tissue; transgenic plant; cereal.
 XX
 XX Pinus radiata.
 XX
 XX WO200055172-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 17-MAR-2000; 2000WO-NZ00031.
 XX

PR 17-MAR-1999; 99NZ-034715.
 XX
 XX (CART-) CARTER HOLT HARVEY LTD.
 XX (TASM-) TASMAN BIOTECHNOLOGY LTD.
 XX (UNMT) UNIV MICHIGAN TECHNOLOGICAL.
 XX
 XX Podila GK, Liu J, Karnosky DF;
 XX
 XX WPI: 2000-594442/56.
 XX N-PSDB: AAA99362, AAA99363, AAA99364.
 XX
 XX Novel plant reproductive tissue promoter, useful to produce plants
 XX which have a diminished reproductive capacity or which are sterile
 XX
 XX Disclosure; Figure 1; 51pp; English.
 XX
 XX This invention relates to a novel plant promoter gene. The promoter is
 XX located in plant reproductive tissue, and the invention includes
 XX transgenic plants containing the promoter. The promoter can be used to
 XX produce plants which have a diminished reproductive capacity or which are
 XX sterile. The constructs can also be used to transform agronomically
 XX important plants in which modulation of reproductive capacity
 XX (particularly the timing and abundance of flowering) is desirable,
 XX e.g. cereals, rice, maize, wheat, barley, oats, rye, soybean and canola.
 XX The present sequence represents the protein encoded by the plant
 XX reproductive promoter (PRAG1) gene of the invention.
 XX
 XX Sequence 222 AA;
 XX

Query Match 34.9%; Score 424.5; DB 21; Length 222;
 Best Local Similarity 50.3%; Pred. No. 1.7e-30;
 Matches 87; Conservative 35; Mismatches 46; Indels 5; Gaps 2;
 QY 1 MGRKIVIRINDNSTQVTFKRRNGIFKAKELALICDAEVLGVTSSTGRLEYEST 60
 DB 1 mgrkviririndnstqvtfkrrngifkakealalicaeavlgsstgrleyest 60
 QY 61 SMKSVIRRYGKAKKEQO--VVANPNSLSEKFWOREAASLRQOLHNLQENYRQLTGDDLSG 117
 DB 61 smksvirrygkakeeqo--vvanpnslsekfworeaslrqolhnlqenyrltgddls 117
 QY 118 LNVKELQSLENQLETSLRGVRRAKDHLLIDETIHDLNRKASLFRHOENTDLYNKI 170
 DB 118 lnvkqlslenqletsrgvrrakdhllidetihdlnrkaslfrhoentdlynkinir 170

Search completed: August 11, 2002, 09:35:57
 Job time: 3512 sec

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OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 07:29:40 ; Search time 208.02 Seconds

(Without alignments)
10564.612 Million cell updates/sec

Title: US-09-970-624-1

Perfect score: 1280
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Scoring table: IDENTITY_NUC
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Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

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Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1109.6	86.7	1268	22	AAAF76058	Maize MADS-box gen
2	1109.6	86.7	1268	22	AAAF7645	Maize ZMMADS2 codi
3	463.4	36.2	5031	22	AAAF76068	Maize MADS-box gen
4	463.4	36.2	5031	22	AAAF76455	Maize MADS2 gene
5	265.6	20.8	687	21	AAAC42918	Arabidopsis thalia
6	254.8	19.9	684	21	AAAC43252	Arabidopsis thalia
7	245	19.1	310	22	AAAF76066	Maize MADS-box gen
8	245	19.1	310	22	AAAF76453	Maize ZMMADS2 gene
9	236.2	18.5	705	21	AAAC42728	Arabidopsis thalia

10	224.2	17.5	717	21	AAAC50308	Arabidopsis thalia
11	188.4	14.7	706	21	AAAC55965	Eucalyptus grandis
12	179.6	14.0	997	17	AAAT34432	Eucalyptus AGE2 cd
13	174.4	13.6	251	22	AAAF76067	Maize MADS-box gen
14	174.4	13.6	251	22	AAAF76454	Maize ZMMADS2 gene
15	171.2	13.4	909	21	AAAG9364	Plant PRG1 promot
16	166.6	13.0	581	21	AAAC57270	Eucalyptus grandis
17	165.8	13.0	1044	20	AAAF71739	Rice OSMADS6 cDNA.
18	158.6	12.4	714	22	AAAF85402	Nucleotide sequenc
19	158.6	12.4	1115	21	AAAF85409	Nucleotide sequenc
20	158.6	12.4	1159	22	AAAF85401	Poplar floral home
21	154.8	12.1	1218	21	AAAC43678	Zea mays DNA fragm
22	150.8	11.8	1321	21	AAAC47718	Zea mays DNA fragm
23	150	11.7	423	21	AAAC56741	OSMADS1 cDNA. Ory
24	149.4	11.7	1143	17	AAAT15919	Petunia hybrida ne
25	146.2	11.4	1157	21	AAAC50201	Petunia nectary-sp
26	146.2	11.4	1157	21	AAAC35494	Nucleotide sequenc
27	142.6	11.1	723	22	AAAF85399	Poplar floral home
28	142.6	11.1	1201	21	AAZ57947	Nucleotide sequenc
29	142.6	11.1	1219	22	AAAF85398	Arabidopsis thalia
30	142.4	11.1	903	21	AAAC51039	Arabidopsis thalia
31	142.2	11.1	777	21	AAAC43464	Arabidopsis thalia
32	142.2	11.1	959	20	AAV99860	Arabidopsis thalia
33	142	11.1	1305	21	AAAC44058	Zea mays DNA fragm
34	141.2	11.0	1494	21	AAAC44550	Zea mays DNA fragm
35	139.8	10.9	434	21	AAAC35822	Zea mays DNA fragm
36	138.4	10.8	1084	17	AAAT34429	Eucalyptus SOE1 cd
37	138	10.8	466	21	AAAC35890	Zea mays DNA fragm
38	137.4	10.7	1178	21	AAAC43696	Zea mays DNA fragm
39	137	10.7	1223	21	AAAC55901	Eucalyptus grandis
40	135.6	10.6	1267	21	AAAC43699	Zea mays DNA fragm
41	134	10.5	1015	21	AAAC51323	Z. mays MADS-box p
42	134	10.5	1134	22	AAAF80396	Nucleotide sequenc
43	134	10.5	1368	22	AAAC84182	A. thaliana, larger
44	133.6	10.4	1342	18	AAAT99437	Maize floral meris
45	133.6	10.4	1345	19	AAV58307	Zea mays Api gene.

ALIGNMENTS

RESULT 1
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ID AAF76058 standard; cDNA; 1268 BP.
XX
AC AAF76058:
XX
DT 22-MAY-2001 (first entry)
XX
DE Maize MADS-box gene ZMMADS2 cDNA, SEQ ID NO:1.
XX
KW Maize MADS box gene; ZMMADS2; pollen-specific expression;
KW Pollen development; function; transgenic plant; male sterility;
KW hybrid seed production; ss.
XX
OS Zea mays.
XX
PN WO200112799-A2.
XX
PD 22-FEB-2001.
XX
PF 16-AUG-2000; 2000WO-EP08002.
XX
PR 18-AUG-1999; 99EP-0116268.
XX
PA (SUED-) SUEDEWESTDEUTSCHE SAAFT200HT.
XX
PI Loerz H, Dresselhaus T, Schreiber D, Heuer S;
XX WPI: 2001-211214/21.
XX P-FSDB; AAF73333.
XX Novel nucleic acid molecule useful for cloning and expressing a pollen

XX Hybridisation assay: genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS *Arabidopsis thaliana*.
XX EPI033405-A2.
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XX 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0131825.
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RESULT 10
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ID AAC50308 standard; DNA: 717 bp.
AC AAC50308;
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DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 64350.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway;
KW Metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Query Match	17.5%;	Score 224.2;	DB 21;	Length 717;
Best Local Similarity	62.6%;	Pred. No. 4.8e-50;		
Matches 374; Conservative	0;	Mismatches 208;	Indels 15;	Gaps 1

RESULT 11

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DT 25-JAN-2001 (first entry)

DE Eucalyptus grandis transcription factor DNA sequence #96.

KM Plant1;transcription factor; gene expression; eucalyptus; pine; acacia
KM Poplar; Sweetgum; teak; mahogany; bZIP; G-box binding factor;
KM basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
KM homeodomain zipper; LIM domain; AP2; ERBBs; zinc finger domain;
KM type 2 CysHis2; CCAAT box element; MYB; ss.

OS Eucalyptus grandis.

PN W0200053724-A2.

PD 14-SEP-2000.

PF 09-MAR-2000; 2000WO-US06112.

PR 11-MAR-1999; 99US-0266513.

XX

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD
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PI Wood M, McGrath A, Shenk MA, Glenn M

Query Match 13.6%; Score 174.4; DB 22; Length 251;
Best Local Similarity 99.4%; Pred. No. 6.6e-37;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 agaagaagtaaaactccgctctatgatgctgaagaactatttcttgaagagatgat 60
QY 1143 actcgaagaagaacatatttgcgcaaggagatttgagatagaaactataatgtaag 1202
|||||
DB 61 actcgaagaagaacatatttgcgcaaggagatttgagatagaaactataatgtaag 120
QY 1203 caataatcttcagaccggaatcggtcgtaattcagaagatgatgctttctca 1258
|||||
DB 121 caataatcttcagaccggaatcggtcgtaattcagaagatgatgctttctca 176

RESULT 15
AAA99364
ID AAA99364 standard; DNA: 909 BP.
XX
AC AAA99364;
XX
DT 22-JAN-2001 (first entry)
XX
DE Plant PrAG1 promoter DNA sequence.
XX
KW Plant promoter; PrAG1; reproductive tissue; transgenic plant; cereal; ds.
XX
OS Pinus radiata.
XX
PN WO200055172-A1.
XX
PD 21-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-N200031.
XX
PR 17-MAR-1999; 99NZ-0334715.
XX
PA (CARTER-) CARTER HOLT HARVEY LTD.
PA (TASM-) TASMAN BIOTECHNOLOGY LTD.
PA (UNMT-) UNIV MICHIGAN TECHNOLOGICAL.
XX
PI Podila GK, Liu J, Karnosky DE;
XX
DR WPI: 2000-594442/56.
XX
PT Novel plant reproductive tissue promoter, useful to produce plants
PT which have a diminished reproductive capacity or which are sterile -
XX
PS Claim 8; Page 39-40; 51pp; English.
XX
CC This invention relates to a novel plant promoter gene. The promoter is
CC located in plant reproductive tissue, and the invention includes
CC transgenic plants containing the promoter. The promoter can be used to
CC produce plants which have a diminished reproductive capacity or which are
CC sterile. The constructs can also be used to transform agronomically
CC important plants in which modulation of reproductive capacity
CC (particularly the timing and abundance of flowering) is desirable,
CC e.g. cereals, rice, wheat, barley, oats, rye, soybean and canola.
CC The present sequence represents DNA encoding the plant reproductive
CC promoter (PrAG1) of the invention.
XX
SQ Sequence 909 BP; 299 A; 172 C; 216 G; 222 T; 0 other.

Query Match 13.4%; Score 171.2; DB 21; Length 909;
Best Local Similarity 59.8%; Pred. No. 9.1e-36;
Matches 306; Conservative 0; Mismatches 203; Indels 3; Gaps 1;
QY 360 atggggagggaggaagatcgatcgacgagatgataactccacgagcggaagtgcacc 419

DB 1 atgggctcglyggaagattgagataaagagatctgaaataactacagaccgaagctact 60
QY 420 ttctccaagcgccggaacggaagcttccaagaaggccaagagctcgacatcctctgcat 479
DB 61 ttctccaagcgccggaagatggtttaaagaagcgatgataattacgttcttctgcat 120
QY 480 gcggaagtcgagcttcgcatcttctccaagcgcgcgctctctacgagtaactagacc 539
DB 121 gcaagaagtcgagcttcgcatcttctccaagcgcgcgctctctacgagtaactagacc 180
QY 540 agcgtgaatcagttatagatcggtacgcaaggc---caagggaagcgcaagctgctc 596
DB 181 agcgtgaaggaagagatctggaaggttacaagaagacttgcgttgaacaacaacaggaagg 240
QY 597 gcaaatcccaactcgcgagcttaagtttggcaaaagggaagcgaagcttgaacaaca 656
DB 241 gcatatcagagctcgaattcagttatggcaacaggaagcgctgtaaacccagacaacag 300
QY 657 ctgcacaacttgcagaagaattatcgcgagttgacggagagatgattcttctggtgcat 716
DB 301 atgacatcttgcacaatgcacaatagacatttgatgggtgacggcttacaagcttgaac 360
QY 717 gtcagaagactgcagctccctggaagaatccaatttgaacaacagcctgcgtggtccgcga 776
DB 361 attaagaagactcaagcaacttgaaggttcgacttgaaaaaaggaatcagcgagtgcatcc 420
QY 777 aagaagaacatctcttgatagatgagatccaagatttgaatcgaaagcgaatttatt 836
DB 421 aaaaagaagcagatggttgcgttgaagagatcgacatcatgagaagaaggaacacatactt 480
QY 837 caccagaagaatatacagactgttaacataagat 868
DB 481 atccagagaatgagattcttcgcaagaagat 512

Search completed: August 11, 2002, 08:42:14
Job time: 4354 sec

Mon Aug 12 08:29:58 2002

us-09-970-624-1.rng

Page 16

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 05:49:44 ; Search time 49.52 Seconds
(without alignments)
6349.170 Million cell updates/sec

Title: US-09-970-624-1

Perfect score: 1280
1 gacgagccgcctgcgcga.....aaaaaaaaaaaaaaaaaaaa 1280

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents.NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	165.8	13.0	1043	2	US-08-867-087B-12
2	149.4	11.7	1141	2	US-08-323-449B-1
3	149.4	11.7	1141	2	US-08-485-981-1
4	149.4	11.7	1141	2	US-08-867-087B-1
5	147.8	11.5	1125	1	US-08-460-512-6
6	142.4	11.1	1457	1	US-08-460-512-1
7	142.2	11.1	959	4	US-09-067-800-7
8	142.2	11.1	959	4	US-09-349-677-7
9	140.8	11.0	1097	1	US-08-460-512-3
10	133.6	10.4	1345	1	US-08-592-214A-7
11	133.6	10.4	1345	3	US-08-659-188-7
12	133.6	10.4	1345	3	US-08-655-227-7
13	133.6	10.4	1345	3	US-08-655-241-7
14	133.6	10.4	1345	3	US-09-149-976-7
15	133.6	10.4	1345	3	US-09-398-326-7
16	129.4	10.1	1027	2	US-08-867-087B-54
17	127.8	10.0	1180	2	US-08-867-087B-16
18	123.8	9.7	896	4	US-09-067-800-5
19	123.8	9.7	896	4	US-09-349-677-5
20	114	8.9	1059	2	US-08-867-087B-14
21	109.6	8.6	945	2	US-08-485-981-9
22	109.6	8.6	945	2	US-08-867-087B-10
23	105.4	8.2	795	3	US-08-904-284-2
24	101	7.9	6138	4	US-09-067-800-4
25	101	7.9	6138	4	US-09-349-677-4
26	95.8	7.5	1500	5	PCT-US93-08386-3
27	95	7.4	1062	4	US-09-067-800-1

28	95	7.4	1062	4	US-09-105-652-1	Sequence 1, Appl
29	95	7.4	1062	4	US-09-349-677-1	Sequence 1, Appl
30	91.6	7.2	2679	3	US-08-904-284-4	Sequence 4, Appl
31	91.4	7.1	5622	4	US-09-067-800-3	Sequence 3, Appl
32	91.4	7.1	5622	4	US-09-349-677-3	Sequence 3, Appl
33	90.4	7.1	1070	4	US-08-904-284-1	Sequence 1, Appl
34	90.2	7.0	756	1	US-08-592-214A-11	Sequence 1, Appl
35	90.2	7.0	756	3	US-08-655-188-11	Sequence 11, Appl
36	90.2	7.0	756	3	US-08-655-227-11	Sequence 11, Appl
37	90.2	7.0	756	3	US-08-655-241-11	Sequence 11, Appl
38	90.2	7.0	756	3	US-09-149-976-11	Sequence 11, Appl
39	90.2	7.0	756	4	US-09-398-326-11	Sequence 9, Appl
40	89.4	7.0	779	3	US-08-592-214A-9	Sequence 9, Appl
41	89.4	7.0	779	3	US-08-655-188-9	Sequence 9, Appl
42	89.4	7.0	779	3	US-08-655-227-9	Sequence 9, Appl
43	89.4	7.0	779	3	US-08-655-241-9	Sequence 9, Appl
44	89.4	7.0	779	3	US-09-149-976-9	Sequence 9, Appl
45	89.4	7.0	779	4	US-09-398-326-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-08-867-087B-12
Sequence 12, Application US/08867087B
Patent No. 5990386
GENERAL INFORMATION:
APPLICANT: An, Gynheung
TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist, LLP
ADDRESSEE: Winston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
City: Portland
State: Oregon
Country: United States of America
Zip: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,087B
FILING DATE: June 2, 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/323,449
FILING DATE: October 14, 1994
APPLICATION NUMBER: U.S. 08/485,981
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-47071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1043 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
US-08-867-087B-12
Query Match 13.0%; Score 165.8; DB 2; Length 1043;

Best Local Similarity 57.7%; Pred. No. 1 5e-35;
Matches 296; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 359 gatgggagggaaagatcgtatccgcaagatgataactccagagccgagcagtgac 418
D 33 gatgggagggaaagatgagtgagtgagccatgagacaaagatcaacagcaggtgac 92
QY 419 ctctccaagcgccggaagggatctcaagaagagccaaagagctgcactctgaga 478
D 93 ctctccaagcgccggaagggatctcaagaagagccaaagagctgcactctgaga 152
QY 479 tgcgagagctgcagctcatctctccagagccgagccctcagagagctcagac 538
D 153 cgccgagagctgcagctcatctctccagagccgagccctcagagagctcagac 212
QY 539 cagcagaaatcagatagatcggtacggaagccaaaggaagagcagcagctgcgc 598
D 213 cgccatmaacaaagcattagaaagcttcaacaaatgtgtgtacaaatgctcaaatgcca 272
QY 599 aaatcccaactcgagcttaagcttggcgaagggagcagcagcttgagacaact 658
D 273 caatgcattcttcaaaactcagacttggtacatgaatgtcaaaagtgaacaaatp 332
QY 659 gcacaactcgaagaaatlatcgagcttgagcagagatgagcttctggtgagatp 718
D 333 tgaagctttgcagcgacactcaaaagcacttgcttgggagagatcttgacactcagct 392
QY 719 caaagaactcagctccctgagagatcaatggaacaaagctgctggtgctgcgcaaa 778
D 393 caaagaactcagctccctgagagatcaatggaacaaagctgctggtgctgcgcaaa 452
QY 779 gaagagaccatctctgtagatgagatcagcagcttgagcgaagagcagcttact 838
D 453 aaagacgcaactgagtgagaaacagctgaggaacttgcgacgaagagcagcttact 512
QY 839 ccaagaaatcacagacttgacaataagatcaa 871
D 513 tgaatttaattaggaactcaagcacaagcttga 545

RESULT 2
US-08-323-449B-1
; Sequence 1, Application US/08323449B
; Patent No. 5859326
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENE CONTROLLING FLORAL DEVELOPMENT AND
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarguist Sparkman Campbell Leigh &
; STREET: Winston
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,449B
; FILING DATE: October 14, 1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-41493
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1141 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: MADS box
; LOCATION: Residues 2-57 of deduced amino acid
; LOCATION: sequence of SEQ ID NO: 1:
; IDENTIFICATION METHOD: Homology to MADS-box proteins
; IDENTIFICATION METHOD: FEATURE:
; NAME/KEY: K-Box
; LOCATION: Residues 90-143 of deduced amino acid
; LOCATION: sequence of SEQ ID NO: 1:
; IDENTIFICATION METHOD: Homology to MADS-box proteins
US-08-323-449B-1

Query Match 11.7%; Score 149.4; DB 2; Length 1141;
Best Local Similarity 57.8%; Pred. No. 4.4e-31;
Matches 344; Conservative 0; Mismatches 241; Indels 10; Gaps 4;

QY 300 tagcgtgcgaagcgagccagaggtcagaagaagagctagctatagcgcgagatcg 359
D 6 tagcgtgcgaagcgagccagaggtcagaagaagagctagctatagcgcgagatcg 64
QY 360 atggggagggagaaagatcgtatcgcaagagctgaactcaagaagcagcgagtgacc 419
D 65 atggggagggagaaagatcgtatcgcaagagctgaactcaagaagcagcgagtgacc 124
QY 420 ttctccaagcgccggaagggatcttcaagaagcgaagagctgcacatcctcgat 479
D 125 ttccgcaagcgccggaagggatcttcaagaagcgaagagctgcacatcctcgat 184
QY 480 gcgagagctgcgctcgtatcttctcaagcagcgccctcagagtagctagc--- 536
D 185 gccgagctgcgctcgtatcttctcaagcagcgccctcagagtagctagc--- 244
QY 537 accagatgaatcagcttatagctgagcagcgaagcgaagcagcagctgcgac 596
D 245 tcatcattgtaaaacacttgagaggtgacgactgcaactcgaactcagagtgca 304
QY 597 gcaaatcccaactcgagcttaagcttggcgaagggaggaagcagcttgaacaaca 656
D 305 gcagctccagaaacagaaatttaatttacc-----aagattacctgagctgaacaaagag 359
QY 657 ctgcaacttgcaagaataatcgcagcttgaagcagtgatgacttctgctgagat 716
D 360 ttgaaatttcttcaaacacacac-acagaaatttcttggtagagatttggccctcactaagc 418
QY 717 gtcaagaagctgcagctcccttgagagatcaatgtgaaagcagctggtgctgcgca 776
D 419 atgaaggagcttgagcagcttgagaaacagatagagatgattccttcaacaaataggtca 478
QY 777 aagaagaccactctctgatatgagatgagatcagatgtgaatcgaagcgaagtgattt 836
D 479 agaaagaaacaaagcagctgcttgatgagctgttgaatggaagacagcagcagcagct 538
QY 837 caccagaagaatacagacttgtaataaagatacactgattgcgaagaataatg 891
D 539 caagattctcaacaaagacttgagaaaaaagttacaggaamaacagctgacagaaatg 593

RESULT 3
US-08-485-981-1
; Sequence 1, Application US/08485981
; Patent No. 5861542
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENE CONTROLLING FLORAL DEVELOPMENT AND

Query Match	11.7%	Score 149.4	DB 2	Length 1141
Best Local Similarity	57.8%	Pred. No. 4,4e-31		
Matches 344	Conservative 0	Mismatches 241	Indels 10	Gaps 4
QY	300	taagctgycgaagcgcgagccaggtgltcaagaagaagctagctatagatcagcgagatcg	359	
Db	6	TACCTTCGAAGAAGGCGATAGTAGTAGAGACAGAGAGAGAGAGAGAGAGAGAGAAAC	-AG 64	
QY	360	atggggagggggaagaatcgtagtccgcagatcgataactccacgagcgcgagtgacc	419	
Db	65	ATGGGGAGGGGGAAGGTGGAGCTGGAAGGGATCGGAACAAGATCACCGCGAGGTGACG	124	
QY	420	tltccaaagcgcgcggaagcggatcttccaagaagcgaagagcgtcgccatcccttcgcat	479	
Db	125	TTGCGCAAGCGCAGGAAGCGCTGCTCAAGAAGGCTTACGAGCTCTCCCTCTCTGCGAC	184	
QY	480	gcggaggtcgcgctcgtaacttctccaaagcgcgcgcgcgctctacgaagtactagc---	536	
Db	185	GCGGAGGTGCGCCCTCATCTCTTCTCCGGCGCGCGCCCTCTCGAGTTCCTCAGGTCA	244	
QY	537	accgaatgaatatcgatatagatcgtgaaagcgccaaggaagaagcagcaatcgctc	596	

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RESULT      4
US-08-867-087B-1
; Sequence 1, Application US/08867087B
; Patent No. 5990386
GENERAL INFORMATION:
APPLICANT: An, Gynheung
TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kiarquist Sparkman Campbell Leigh &
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,087B
FILING DATE: June 2, 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/323,449
FILING DATE: October 14, 1994
APPLICATION NUMBER: U.S. 08/485,981
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-47071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1141 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
; US-08-867-087B-1

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11.78; Score 149.4; DB 2; Length 1141;


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Db 202 GTTACTCAAGAAAGCTTATGAGCTCTGCTGTGTGTGAGAGCTAGGTTGGCTTTGCA 261
QY 499 tcttccagcagccgcgcctctcaggtacttagaagcaagatgaatcagttatag 558
Db 262 TCTTCTCCACTGAGGCGCTCTCTAGAGTAGCCACACAGAGTGTGAGAGAACATAG 321
QY 559 atcgttacggcaagc---caaggaagagcagcagctgcgcgaattcccaactcgcgc 615
Db 322 AAAGGTACAGAAAGCTTGTCTCCGACGCCGTTAACCTCCGACATCCAGGCTATTA 381
QY 616 ttaagtttggcaaaaggagcagcagcttgagacaacactgacacttgaagaa 675
Db 382 CTCACACTACTATCAGCAAGAGGCGCTTAAACCTCCGACAGACATCCGACATTCAGANT 441
QY 676 attatcgagcagttgacggagatgacttcttgagctgaatgaatgaatcagtc 735
Db 442 TGAACAGACACTTTTGTGTGATCTTTGCTCTTGAACCTTAAAGGAACTCAAGAAC 501
QY 736 tggagaatcaattggaacaagcctgcgtggtgctgcgcgaagaaagacatcttga 795
Db 502 TTGAAGTAGGCTTGAGAAAGGAATCACTGCTGCCATCCAGAGACGACAGATGTTAG 561
QY 796 tagatgaattcagcagatttgaaatcgaaagcagttatttccaccaagaatacagact 855
Db 562 TTGCAGAGATTGAATACATGCAAAAAGGAATGACAGCTGCAAAACGATTAATCATC 621
QY 856 tgaacaataagatca 870
Db 622 TCCGCTCCAGATTA 636

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RESULT 8

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US-09-349-677-7
; Sequence 7, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ. ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 959 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 78..818
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..959
; OTHER INFORMATION: /note="AGL5 cDNA and deduced
; OTHER INFORMATION: protein sequences."
; US-09-349-677-7

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Query Match 11.1%; Score 142.2; DB 4; Length 959;
Best Local Similarity 54.8%; Pred. No. 3,6e-29;
Matches 304; Conservative 0; Mismatches 248; Indels 3; Gaps 1;

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QY 319 aggtcaagaagagactagactagatagccggagatcgatgggagggagaatcg 378
Db 82 AGGGTGGTGGAGTATGAAAGTAGCAGAGACGACGAAGAAGATAGGAGAGGAAATAG 141
QY 379 tgatccgagatcgatgaactccagcagcgcaggtgaccttccaaagcgcggaagc 438
Db 142 AGATTAAGAGGATGAGAAACACTACGAATGTCACACTTTCTCCAAACGACGCAATG 201
QY 439 ggaattcgaagagcgaagagctgcacatcctctcgatgagatgcgagatcgctcga 498
Db 202 GTTACTCAAGAAAGCTTATGAGCTCTCTGTGTGTGACGCTGAGGTTGCTTTGCA 261
QY 499 tcttccagcagccgcgcctctcaggtacttagacacagcagcatgaatcagttatag 558
Db 262 TCTTCTCCACTGAGGCGCTCTCTAGAGTAGCCACACAGATGAGGAGGAACATAG 321
QY 559 atcgttacggcaagc---caaggaagagcagcagctgcgcgaattcccaactcgcgc 615
Db 322 AAAGGTACAGAAAGCTTCTCCGACGCCGTTAACCTCCGACATCCAGGCTATTA 381
QY 616 ttaagtttggcaaaaggagcagcagcttgagacaacactgacacttgaagaa 675
Db 382 CTCACACTACTATCAGCAAGAGGCGCTTAAACCTCCGACAGATTCGATTCGAAAT 441
QY 676 attatcgagcagttgacggagatgacttcttgagctgaatgacaaactgcagtc 735
Db 442 TGAACAGACACTTTTGTGTGATCTTTGCTCTTGAACCTTAAAGGAACTCAAGAAC 501
QY 736 tggagaatcaattggaacaagcctgcgtggtgctgcgcgaagaaagacatcttga 795
Db 502 TTGAAGTAGGCTTGAGAAAGGAATCAGTCCGATCCAAAGACGACAGATGTTAG 561
QY 796 tagatgaattcagcagatttgaaatcgaaagcagttatttccaccaagaatacagact 855
Db 562 TTGCAGAGATTGAATACATGCAAAAAGGAATGACAGCTGCAAAACGATTAATCATC 621
QY 856 tgaacaataagatca 870
Db 622 TCCGCTCCAGATTA 636

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RESULT 9

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US-08-460-512-3
; Sequence 3, Application US/08460512
; Patent No. 5744693
; GENERAL INFORMATION:
; APPLICANT: MEYEROWITZ, Elliot M.
; APPLICANT: YANOFKY, Martin F.
; APPLICANT: MA, Hong
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecaulin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California

```


US-08-659-188- /	
Query Match	10.48; Score 133.6; DB 3; Length 1345;
Best Local Similarity	57.5%; Pred. No. 9.3e-27;
Matches 300; Conservative	0; Mismatches 214; Indels 8; Gaps 3

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; TELECOMMUNICATION INFORMATION
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 base pairs

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; TELECOMMUNICATION INFORMATION
;
; TELEPHONE: (619) 535-9001
;
; TELEFAX: (619) 535-8949
;
; INFORMATION FOR SEQ ID NO: 7:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 1345 base pairs

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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays Apl. "
US-08-655-227-7

Query Match 10.4%; Score 133.6; DB 3; Length 1345;
Best Local Similarity 57.5%; Pred. No. 9.3e-27;
Matches 300; Conservative 0; Mismatches 214; Indels 8; Gaps 3;

QY 348 gcccggagatcgatgggaggggaaagatcgtgacccggagatcgatcgaatccagcagc 407
DB 137 GGCACACAGGCGATGGCGCGGACAGGTACAGCTGAAGCGATAGAACACAGATAAAC 196
QY 408 cggcagtgatccctcctcaagcgcggaacggaatcttcaagaagccaaagagctgcc 467
DB 197 CGCAGGAGTACTTCTCCAAAGCGCGCGCTGCTCAAGAAAGCGGACAGATCTCC 256
QY 468 atccctgagatcgagaggtcgccctgcatcttccagaccggccgctctacgag 527
DB 257 GTCTCTGCGATGCGGAGGTCGCGCTCATCGTCTTCCGCCCAAGGCGCAACCTCTACGAG 316
QY 528 tactcta---gcaccagatgaatcagttatagatcggtacggaagggccaaagaagag 584
DB 317 TACGCCACCGACTCCGCGATGACAAATTTCTGAACCGCTATGAGCGATATTCCTATGCT 376
QY 585 cagcaagtcgctgcgaatcccaactcgagacttaagt-----ttggcaagggagagcagc 640
DB 377 GAAAGGCTCTTATTTCAGCTGGAATCTGAAGTGAGGGAATTTGGTGCACGAAATACAGG 436
QY 641 aagcttgagacaacaactgcgaacttgcgaagaataatcagcagttgacgagatga 700
DB 437 AAACCTGAAGGCCAAATATG-AGACCATACAAATAATGCCACACCTGATGGGAGAGGA 495
QY 701 tcttcttgagtgatgcaagaaactcagtcctcgtgagaaatcaattggaaacaagcct 760
DB 496 TCTAGAGCTTTGAATCCCAAGAGAGCTCCAGCAACTAGACAGCAAGCTGGAAGCTCACT 555
QY 761 gctggtgctcgcgcaagaaggaagaccatctctgtatagatgagatcagaattgaatcg 820
DB 556 GAAGCAGATGATCAAGAGAGAGGACCTTATGGCGAGTCTATTCTGAGCTACAGAA 615
QY 821 aaagcaagttatttccacagaataatcagactgttaca 862
DB 616 GAAGGAGAGTCACTGCAAGAGAGAGCAAGGCTCTGAGAA 657

RESULT 13

US-08-655-241-7
Sequence 7, Application US/08655241
Patent No. 6025543
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Weigel, Detlef
TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
TITLE OF INVENTION: Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,241
FILING DATE: 05-JUN-1996
CLASSIFICATION: CLASS 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays Apl. "
US-08-655-241-7

Query Match 10.4%; Score 133.6; DB 3; Length 1345;
Best Local Similarity 57.5%; Pred. No. 9.3e-27;
Matches 300; Conservative 0; Mismatches 214; Indels 8; Gaps 3;

QY 348 gcccggagatcgatgggaggggaaagatcgtgacccggagatcgatcgaatccagcagc 407
DB 137 GGCACACAGGCGATGGCGCGGACAGGTACAGCTGAAGCGGATAGAACACAGATAAAC 196
QY 408 cggcagtgatccctcctcaagcgcggaacggaatcttcaagaagccaaagagctgcc 467
DB 197 CGCAGGAGTACTTCTCCAAAGCGCGCGCTGCTCAAGAAAGCGGACAGATCTCC 256
QY 468 atccctgagatcgagaggtcgccctgcatcttccagaccggccgctctacgag 527
DB 257 GTCTCTGCGATGCGGAGGTCGCGCTCATCGTCTTCCGCCCAAGGCGCAACCTCTACGAG 316
QY 528 tactcta---gcaccagatgaatcagttatagatcggtacggaagggccaaagaagag 584
DB 317 TACGCCACCGACTCCGCGATGACAAATTTCTGAACCGCTATGAGCGATATTCCTATGCT 376
QY 585 cagcaagtcgctgcgaatcccaactcgagacttaagt-----ttggcaagggagagcagc 640
DB 377 GAAAGGCTCTTATTTCAGCTGGAATCTGAAGTGAGGGAATTTGGTGCACGAAATACAGG 436
QY 641 aagcttgagacaacaactgcgaacttgcgaagaataatcagcagttgacgagatga 700
DB 437 AAACCTGAAGGCCAAATATG-AGACCATACAAATAATGCCACACCTGATGGGAGAGGA 495
QY 701 tcttcttgagtgatgcaagaaactcagtcctcgtgagaaatcaattggaaacaagcct 760
DB 496 TCTAGAGCTTTGAATCCCAAGAGAGCTCCAGCAACTAGACAGCAAGCTGGAAGCTCACT 555
QY 761 gctggtgctcgcgcaagaaggaagaccatctctgtatagatgagatcagaattgaatcg 820
DB 556 GAAGCAGATGATCAAGAGAGAGGACCTTATGGCGAGTCTATTCTGAGCTACAGAA 615
QY 821 aaagcaagttatttccacagaataatcagactgttaca 862
DB 616 GAAGGAGAGTCACTGCAAGAGAGAGCAAGGCTCTGAGAA 657

RESULT 14
US-09-149-976-7
; Sequence 7, Application US/09149976
; Patent No. 6127123
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; City: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/149,976
; FILING DATE: 09-SEP-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,214
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 3291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ. ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 149..968
; NAME/KEY: misc.feature
; LOCATION: 1..1345
; OTHER INFORMATION: /note="product = Zea mays API"
US-09-149-976-7

Query Match 10.4%; Score 133.6; DB 3; Length 1345;
Best Local Similarity 57.5%; Pred. No. 9.3e-27;
Matches 300; Conservative 0; Mismatches 214; Indels 8; Gaps 3;
QY 348 ggcgcgaagatcgatgggaggaagatcgatgcgcgaagatcgataactccacgagc 407
DB 137 ggcgaacaaagcgtggcgccgcaaggtacagctgaacgagatagagaaacaaagtaaac 196
QY 408 cggcgaagtgacctcttccaaagccggaacggatcttcaagaagcccaagagctgcgc 467
DB 197 cggcgaagtgacctcttccaaagccggaacggatcttcaagaagccgacgacgacgtcc 256
QY 468 atccctcgatcgagaggtcgccctcgatcactctctccaaagccgacgacgacgtccag 527
DB 257 gtctctcgatcgagaggtcgccctcgatcactctctccaaagccgacgacgacgtccag 316
QY 528 tactctctctcgcacgaagatgaatcagttatagatcggtacgcaagcccaaggaagag 584
DB 317 tacgctcaccgacgacgtccgacgacgacgacgacgacgacgacgacgacgacgacgac 376
QY 585 cagcaagtcgtcgcaaatcccaactcgagcttaagctcttgagcaaggaagcagc 640

DB 377 gaaaagcgtcttatttcagctgaatctgaagtgaggaattgtgctccacgacgtatcagc 436
QY 641 aagcttgagacaacaactgcacacttgcagaataattatcgcaagttgacgagatga 700
DB 437 aaactgaagggccaaatttg-acaccatcacaataaaagccacacccgattggagagca 495
QY 701 tcttcctgagctgaatgcagaagactcagtccttcgagagatcaattggaacaagcct 760
DB 496 tcttagagctttgaaatcccaaaagactccagacacttagagcagacgctgagttact 555
QY 761 gctgtgtgtccgcgcaagaagacatctctgatatagatgaattcaagttgacgc 820
DB 556 gaagacatcagatcagaagagagagccaccttatggccgacgactattctgacgtacagaa 615
QY 821 aaagcgaagttatttccacgaagaataacagacttgaaca 862
DB 616 gaagagaggtcactgcagagagagaaacacgcttcgacgaa 657

RESULT 15
US-09-398-326-7
; Sequence 7, Application US/09398326
; Patent No. 6355863
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; REPRODUCTIVE DEVELOPMENT AND METHODS OF MAKING SAME
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell and Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; City: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/398,326
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/659,188
; FILING DATE: 05-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 3739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ. ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 149..968
; NAME/KEY: misc.feature
; LOCATION: 1..1345
; OTHER INFORMATION: /note="product = Zea mays API."
US-09-398-326-7

Query Match 10.4%; Score 133.6; DB 4; Length 1345;

Best Local Similarity 57.58; Pred. No. 9.3e-27;
Matches 300; Conservative 0; Mismatches 214; Indels 8; Gaps 3;

OY	348	gcccgaatcgaatggggaggggaaatacgtgtccgaagtatcgaatactccacagc	407
Db	137	gscacacaaaggcgnhgccgccgcgaagctacacgtgaaagccgatagcaaacaaatAAC	196
OY	408	cgcgaatgacccctccaaagcgcggaacggatctctcaaaagacgaagagctgc	467
Db	197	cgccagcgcgacctctccaaacgcgcgaacgcgcctgctcaaaagcgcgcacgagatcc	256
OY	468	atccctctcgaatgcgaagctgcgctgcatactctccaaagccgcgcgcctcgaag	527
Db	257	gtccctctcgatggccgaagtcgccgtatcgtcttcttcccccagggcaagctctACAG	316
OY	528	tactcta---gcaccagatgaatacagtatagatcgtacgcgaagccaaagaaag	584
Db	317	TACGCGACCGACCTCCCGATGACAAAAATCTTGAACGCTATGAGCATTTCTCTATGT	376
OY	585	cagcaagtcgcgcgaatacccaactcgtgagcttaagc-----ttggcaagagagcagc	640
Db	377	GA AAAAGCTCTTATTTTCAGCTGGAATTCGAAATGAGGAAATTTGTGCCAGATACAGG	436
OY	641	aagcttgacacaacaactgcacaacttgcagaanaattatcgcgaattgcacggagatga	700
Db	437	AAACTGAAGGCCCAAAATTTG-AGACCAATACAAAATGCCACAGACACTGATGGGAGGA	495
OY	701	tcttctcgtgagctgaatgtcaaaagactgcagctcccttggagaalccaattgaaacaagcct	760
Db	496	TCTAGAGCTTTGAAATCCCAAGAGCTCCAGCAATGAGACACAGCTGGATAGCTCACT	555
OY	761	gcgttgatgtccgcgaagaagaagcactctcttgatagatcgaagatcaacatttgaatcg	820
Db	556	GAAAGCATCTGAGATCAAGGAAGAGACCCTTATGGCCGAGTCTATTTCAGCTACAGAA	615
OY	821	aaaggcaagttattttacccaagaanaatacaagacttgttaaca	862
Db	616	GAAAGAGAGTCACTCGAGGAGGGAACAAGGCTTGCACAA	657

Search completed: August 11, 2002, 08:38:22
Job time: 10118 sec

4

5

6

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 05:46:56 ; Search time 1691.01 Seconds
(without alignments)
10216.440 Million cell updates/sec

Title: US-09-970-624-1

Perfect score: 1280

Sequence: 1 gacagcagccgcctgcgcga.....aaaaaaaaaaaaaaaa 1280

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estri:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
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12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	569.4	44.5	614	9	AN453286 660039F01
2	544.6	42.5	608	9	AM067614 61404610
3	377.6	29.5	434	9	AI947410 614044G10
4	333.2	26.0	468	9	AM053261 614073H05
5	269	21.0	463	10	BE354988 DGI 10.H0
6	263.6	20.6	716	10	BM405213 EST575540
7	253	19.8	632	9	AM216280 EST303461
8	246	19.2	812	9	BE034403 MH04D03 M
9	245.8	18.2	553	10	BE592879 EST491557
10	237.6	18.6	487	9	AI974336 T110185e
11	236.5	18.5	499	10	BM323459 PIC1 19.E
12	230.8	18.0	581	10	BE596704 P11 58.F0
13	226	17.7	492	9	AI389596 MRC56A01
14	213.6	16.7	598	9	AW706936 SK08D08.Y
15	212.2	16.6	587	10	BE445262 WHE1133_A
16	175.4	13.7	649	9	AM184799 SE82F12.Y
17	173.6	13.6	786	9	BE195464 HVSMEH008

18	173.6	13.6	892	10	BC415259
19	173.2	13.5	507	9	AM705451
20	172.8	13.5	635	9	AI995037 701501560
21	168.2	13.1	422	10	BE341755
22	167	13.0	482	10	BE319808
23	166.6	13.0	698	10	BE659915
24	165.8	13.0	507	10	BE319610
25	165.4	12.9	455	10	BC651806
26	163.8	12.8	558	9	AM705789
27	163.4	12.8	608	9	AM278878
28	162.8	12.7	493	10	BE423660
29	162.8	12.7	597	9	AM704750
30	161.4	12.6	543	10	BE659914 4-C1 Gmax
31	160.6	12.5	613	10	BE659913 3-D9 Gmax
32	159.4	12.5	804	10	BC414586
33	157.4	12.3	960	10	BC445265
34	156.2	12.2	863	10	BI958127
35	155.6	12.2	700	9	AL509053
36	155.2	12.1	566	9	AI728519
37	154.8	12.1	872	10	BE456120
38	154.6	12.1	726	10	BE430838
39	154.2	12.0	481	10	BE610259
40	154.2	12.0	700	9	AL506480
41	154	12.0	584	10	BC442607 GA_Ea001
42	153.6	12.0	512	10	BC367358
43	153.6	12.0	561	10	BM324399
44	152.8	11.9	754	10	BI311053
45	152.8	11.9	916	10	BE454527

ALIGNMENTS

RESULT 1
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DEFINITION 660039F01.y1 660 - Mixed stages of anther and pollen Zea mays cDNA,
LOCUS
ACCESSION AM453286
VERSION AM453286.1 GI:6994072
KEYWORDS
SOURCE Zea mays.
ORGANISM Zea mays.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 660039 row: F column: 01.
Location/Qualifiers
1. 614
/organism="Zea mays"
/cultivar="Ohio43"
/db_xref="taxon:4577"
/clone_lib="660 - Mixed stages of anther and pollen"
/tissue_type="whole premeiotic anthers to pollen shed"
/dev_stage="premeiotic anthers to pollen shed"
/lab_host="XLR"
/note="Organ: anthers; Vector: Lambda Zap; Site:1: Ecotri;
Site:2: XhoI; Anther and pollen cDNA library.
Directionally sequenced with 5' end at the Ecotri site.
Created by Amie Franklin."

BASE COUNT

213 a 113 c 139 g 149 t

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 434)

JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences

FEATURES	Location/Qualifiers
source	1. .434

BASE COUNT	123 a	95 c	69 g	145 t	2 others
ORIGIN					

RESULT	4				
AM053261/c					
LOCUS	AM053261	468 bp	mRNA	linear	EST 20-SEP-1999
DEFINITION	614073h05.x1 614 -	root	cdna	library from	walbot lab zea mays
					cdna
ACCESSION	AM053261				
VERSION	AM053261.1				
KEYWORDS	Est.				
SOURCE	zea mays.				

ORGANISM *Zea mays*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; *Zea*.
 1 (bases 1 to 468)

JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V

FEATURES	Location/Qualifiers
source	1. .468

BASE COUNT	139 a	102 c	77 g	148 t	2 others
ORIGIN					

RESULT	5	463 bp	mrna	linear	EST 20-JUL-2000
LOCUS	BE354988				
DEFINITION	DG1.10.H09.bl_A002 Dark Grown 1 (DG1) Sorghum bicolor cDNA, mRNA sequence.				
ACCESSION	BE354988				
VERSION	BE354988.1	GI:9296098			
KEYWORDS	EST.				
SOURCE	Sorghum.				
ORGANISM	Sorghum bicolor				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				

RESULT 7
 LOCUS AM218280 632 bp mRNA linear EST 18-MAY-2001
 DEFINITION EST03461 tomato radicle, 5 d post-imbibition, Cornell University
 Lycopersicon esculentum cDNA clone cLEZ6G19 similar to Medicago
 sativa MADS-box protein, mRNA sequence.
 ACCESSION AM218280
 VERSION AM218280.1 GI:6529154
 KEYWORDS EST.
 SOURCE tomato.
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 Lycopersicon.
 1 (bases 1 to 632)
 van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Liang,F.,
 Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,
 Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
 Generation of ESTs from tomato radicle tissue
 Unpublished (1999)
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
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 1. .632
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="cLEZ6G19"
 /clone_lib="tomato radicle, 5 d post-imbibition, Cornell
 University"
 /tissue_type="radicle"
 /dev_stage="seedlings 5 days post-imbibition"
 /note="vector: pBlueScript SK(-); Site1: EcoRI; Site2:
 XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin
 (USDA-ARS, Ithaca, NY 14850)."
 BASE COUNT 192 a 112 c 171 g 157 t
 ORIGIN

Query Match 19.8%; Score 253; DB 9; Length 632;
 Best Local Similarity 73.7%; Pred. No. 9.5e-32;
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QY 358 cgatgggaggggaaagatcgatccgagatcgataactcacagccgagcagatga 417
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QY 418 cctctccaagccgagcggatcttcaagaagcccaagagctcgccatcctctg 477
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 Db 256 CGTCTCGAAGAGAGAAATGATGCTGAAGAGGCGCAAGGAGCTAGGATTTCTGCG 315

QY 478 atggcgaggtcgccctcgatcctctccagaccgagccgctctcaagatctctaga 537
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 Db 316 ATGCGAGGCGCGAGTTATTTATCTTCGATCTCGATCTGAAACTCTATGAATTTCAAA 375

QY 538 ccagcatgaatcaagtataatcgtaacgcaagcccaagaagaagcagcagtcgtc 597
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QY 658 tgcacacatgcaagaanaattatcgacgttgacggagatgatcttctggctgaatg 717
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 Db 496 TTCAGACTTGGCAAGATCACCGCAAAATGATGGTGAGGAACCTTCTGTGAGCG 555

QY 718 tcaagaactgcagtccttgagagaatcaattggaaaacagcctcgtgglytccgcgca 777
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QY 778 agaagaccatctcttg 794
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RESULT 8
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 LOCUS BE034403
 DEFINITION MH04D03 MH Mesembryanthemum crystallinum cDNA 5' similar to
 mads-box protein agl17-like protein, mRNA sequence.
 ACCESSION BE034403
 VERSION BE034403.1 GI:8329412
 KEYWORDS EST.
 SOURCE common ice plant.
 ORGANISM Mesembryanthemum crystallinum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
 1 (bases 1 to 812)
 Bohnerl,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M., Ferreira
 ,H., Kawasaki,S., McCollough,A., Michalowski,C.B., Palacio,C.,
 Scara,G., Wheeler,M. and Zepeda,G.R.
 Functional Genomics of Plant Stress Tolerance
 Unpublished (2000)
 COMMENT Contact: Michalowski,C.B.
 University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: cbm@u.arizona.edu
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 Best Local Similarity 68.7%; Pred. No. 1.2e-30;
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QY 478 atggcgaggtcgccctcgatcctctccagaccgagccgctctcaagatctctaga 537
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QY 538 ccagcatgaatcaagtataatcgtaacgcaagcccaagaagaagcagcagtcgtc 597
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 LOCUS 598 bp mRNA linear EST 03-DEC-2001
 DEFINITION sk08d08.y1 Gm-cl023 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 Gm-cl023-3496 5' similar to TR:049351 049351 ANRI , MADS-BOX
 PROTEIN. ; mRNA sequence.
 ACCESSION AM706936
 VERSION AM706936.1 GI:7591198
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 598)
 REFERENCE Shoemaker, R., Kelm, P., Vodka, L., Erpelting, J., Coryell, V., Khanna
 A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
 Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
 R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
 R., Waterson, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)
 CONTACT Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: ccu@resgen.com
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 /lab_host="DH10B"
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 library was prepared using the life technologies
 pSuperScript cDNA library construction kit. Complementary
 DNA was synthesized from mRNA using a poly (dt) sequence
 with a Not I restriction site. Sal I linkers adapters
 were ligated to the blunt-ended cDNA fragments followed by
 Not I digestion. The cDNA fragments were directionally
 cloned into the Not I-Sal I restriction site of the
 pSPORT1 vector. The ligated cDNA fragments were
 transformed into E.coli Electromax DH10B host cells. This
 library was constructed by Dr. Lila Vodka and Dr. Anu
 Khanna."
 BASE COUNT 189 a 117 c 138 g 153 t 1 others

ORIGIN
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 Best Local Similarity 65.9%; Pred. No. 2,4e-25;
 Matches 309; Conservative 0; Mismatches 160; Indels 0; Gaps 0;
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 DB 130 GATGGGGGAGAGTAAGATTGGATTGCAAGATGAGACACTCCACTGCGGTCAAGTGAC 189
 QY 419 ctctccagcgcgcgaagcgaagcgaagcgaagcgaagcgaagcgaagcgaagcgaagcga 478
 DB 190 TTTCTCGAAGAGAGAAATATGATTCCTTAAGAAAGCTAGAGAAATTTGCTTTTGTGA 249
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 DB 250 TGCTGAAGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTG 309
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 QY 599 aatcccaactcgcgaagcgaagcgaagcgaagcgaagcgaagcgaagcgaagcgaagcga 658
 DB 370 GAATCCGGCTTCACAGCGAAGTTTGGACAGACAGACAGACAGACAGACAGACAGACAGCT 429
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 QY 779 gaagaccatctctgatatagatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 827
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 library Trilicium aestivum cDNA clone WHE1133_A05_A09, mRNA
 sequence.
 ACCESSION BE445262
 VERSION BE445262.1 GI:9444818
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Trilicium aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triliceae; Trilicium.
 1 (bases 1 to 587)
 REFERENCE Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
 P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T.,
 Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.
 The structure and function of the expressed portion of the wheat
 genomes - Normalized root cDNA library
 Unpublished (2000)
 CONTACT: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105957773
 Fax: 5105959818
 Email: oanderson@pw.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: StrataGene SK primer.
 Location/Qualifiers
 1. 587
 FEATURES
 source

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/cultivar="Chinese Spring"
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 nystatin and cefotaxime in covered crystallization
 dishes. Roots were harvested. The tissue, total RNA, and
 poly(A) RNA were prepared, a cDNA library was made in the
 t11 clone lab (Choi, Close, Fenton) at the University of
 California, Riverside. The cDNA clones were in vivo
 excised to give bluescript phagemids before
 normalization was carried out. The mass excision of
 phagemid library and normalization were done in HT Nguyen
 lab by D. Zhang at Texas Tech University. Normalization
 protocol used was that of Soares. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors).".

BASE COUNT	175 a	134 c	167 g	111 t
ORIGIN				

Query Match	16.6%;	Score 212.2;	DB 10;	Length 587;
Best Local Similarity	71.0%;	Pred. No. 4.1e-25;		
Matches 296;	Conservative	0;	Mismatches 118;	Indels 3;
				Gaps 14.

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Oy	596	cgcaatcccaactcggagcttaagttctgcaaaaggaaggaacgaagcttgagacaca	655
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Oy	656	actgcacaactgcagaanaattatcggcagttgaacggagatgatctcttcgtgctgaa	715
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Search completed: August 11, 2002, 08:05:38
Job time: 8322 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 11, 2002, 08:38:25 ; Search time 24.9 Seconds
(Without alignments)
235,427 Million cell updates/sec

Title: US-09-970-624-2
Perfect score: 1216
Sequence: 1 MGRGKIVIRINDSTRQVT.....POONTEPSTAKLGQLRP 240

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	426.5	35.1	285	1	US-08-460-512-2 Sequence 2, Appli
3	418.5	34.4	252	1	US-08-460-512-4 Sequence 4, Appli
4	417	34.3	246	4	US-09-067-800-8 Sequence 8, Appli
5	417	34.3	246	4	US-09-349-677-8 Sequence 8, Appli
6	409.5	33.7	248	1	US-08-460-512-7 Sequence 7, Appli
7	405	33.3	248	4	US-09-067-800-6 Sequence 6, Appli
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10	393	32.3	253	3	US-08-592-214A-4 Sequence 4, Appli
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22	388	31.9	255	3	US-08-655-241-6 Sequence 6, Appli
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ALIGNMENTS

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RESULT 1
US-08-460-512-5
; Sequence 5, Application US/08460512
; Patent No. 5744693
GENERAL INFORMATION:
APPLICANT: MEYEROWITZ, Elliot M.
APPLICANT: YANOFSKY, Martin F.
TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Richard F. Trecartin
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,512
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/293,278
FILING DATE:
APPLICATION NUMBER: US/07/956,694
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57322/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-512-5
Query Match 35.1%; Score 426.5; DB 1; Length 252;
Best Local Similarity 41.1%; Pred. No. 6.6e-33;

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[illegible]

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1      RESULT# 2
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3      ; Sequence 2, Application US/08460512
4      ; Patent No. 5744693
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: MEYEROWITZ, Elliot M.
8      ; APPLICANT: YANOFSKY, Martin F.
9      ; APPLICANT: MA, Hong
10     ; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
11     ; NUMBER OF SEQUENCES: 7
12     ; CORRESPONDENCE ADDRESS:
13     ; ADDRESSEE: Richard F. Treccartin
14     ; STREET: 4 Embarcadero Center, Suite 3400
15     ; CITY: San Francisco
16     ; STATE: California
17     ; COUNTRY: USA
18     ; ZIP: 94111
19     ;
20     ; COMPUTER READABLE FORM:
21     ; MEDIUM TYPE: Floppy disk
22     ; COMPUTER: IBM PC compatible
23     ; OPERATING SYSTEM: PC-DOS/MS-DOS
24     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
25     ; CURRENT APPLICATION DATA:
26     ; APPLICATION NUMBER: US/08/460,512
27     ; FILING DATE:
28     ; CLASSIFICATION: 800
29     ; PRIOR APPLICATION DATA:
30     ; APPLICATION NUMBER: US/08/293,278
31     ; FILING DATE:
32     ; APPLICATION NUMBER: US/07/956,694
33     ; FILING DATE:
34     ; ATTORNEY/AGENT INFORMATION:
35     ; NAME: Treccartin, Richard F.
36     ; REGISTRATION NUMBER: 31,801
37     ; REFERENCE/DOCKET NUMBER: A-57322/RFT
38     ; TELECOMMUNICATION INFORMATION:
39     ; TELEPHONE: (415) 781-1989
40     ; TELEFAX: (415) 398-3249
41     ; INFORMATION FOR SEQ ID NO: 2:
42     ; SEQUENCE CHARACTERISTICS:
43     ; LENGTH: 285 amino acids
44     ; TYPE: amino acid
45     ; TOPOLOGY: linear
46     ; MOLECULE TYPE: protein
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48     ; US-08-460-512-2

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Query Match	35.1%;	Score 426.5;	DB 1;	Length 285;
Best Local Similarity	41.1%;	Pred. No. 7.9e-33;		
Matches 102;	Conservative 49;	Mismatches 74;	Indels 23;	Gaps 7

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OY      2  GGGKIVIRIDINSTRQVYFESRRNGIFRKKKEKELIICDAEVLGVYFSTGRLYEYSTS 61
Db      51  GGGKIEIRIENIETTRQYTFECCRNRGGLAKKAYELSVLCDAEVALIVSSRRRLIYEYSNS 110
OY      62  MKSVTDTRYGKAKEEQ---VYANPNSELKEMOREAASLIRQOLAHNLQENYRQYLTGDDLSGL 118
Db      111  VKGIEREKKAISDMSNTGSVAELINAO---YYQOESAKIRQOIIISONSNRQIMQETIGSM 166
OY      119  NKEKLOSLLENQLETSLRGVRAKKIDHLIDETIHDLNIRKASLPHOENPTDLYNKTNILIREOND 176
Db      169  SKPELRNIEGRERISITIRSKKNKLLFSELDYQMKRRVYDLAHNNOILRAKI-----AENE 222
OY      179  ELHKKIYTEEGDPCVYNRSPPPPNFVAVETEDVPVO---TELSTLPOQNNIEPSTA--- 231
Db      225  RNNPSISLMPGSGNYEOLMPP-----QIOSQPFDSRNFYQVAAL-QPNNNHHSSAGRQ 277
OY      232  PRIGIQLI 239
Db      278  DQYALQIV 285

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1      RESULT      3
2      US-08-460-512-4
3      ; Sequence 4, Application US/08460512
4      ; Patent No. 5744693
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: MEYEROWITZ, Elliot M.
8      ; APPLICANT: YANOFSEKY, Martin F.
9      ; APPLICANT: MA, Hong
10     ; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
11     ; NUMBER OF SEQUENCES: 7
12     ;
13     ; CORRESPONDENCE ADDRESS:
14     ; ADDRESSEE: Richard F. Trecartin
15     ; STREET: 4 Embarcadero Center, Suite 3400
16     ; CITY: San Francisco
17     ; STATE: California
18     ; COUNTRY: USA
19     ; ZIP: 94111
20     ;
21     ; COMPUTER READABLE FORM:
22     ; MEDIUM TYPE: Floppy disk
23     ; COMPUTER: IBM PC compatible
24     ; OPERATING SYSTEM: PC-DOS/MS-DOS
25     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
26     ;
27     ; CURRENT APPLICATION DATA:
28     ; APPLICATION NUMBER: US/08/460,512
29     ; FILING DATE:
30     ; CLASSIFICATION: 800
31     ; PRIOR APPLICATION DATA:
32     ; APPLICATION NUMBER: US/08/293,278
33     ; FILING DATE:
34     ; APPLICATION NUMBER: US/07/956,694
35     ; FILING DATE:
36     ; ATTORNEY/AGENT INFORMATION:
37     ; NAME: Trecartin, Richard F.
38     ; REGISTRATION NUMBER: 31,801
39     ; REFERENCE/DOCKET NUMBER: A-57322/RTT
40     ; TELECOMMUNICATION INFORMATION:
41     ; TELEPHONE: (415) 781-1989
42     ; TELEFAX: (415) 398-3249
43     ; INFORMATION FOR SEQ ID NO: 4:
44     ; SEQUENCE CHARACTERISTICS:
45     ; LENGTH: 252 amino acids
46     ; TYPE: amino acid
47     ; TOPOLOGY: linear
48     ;
49     ; MOLECULE TYPE: protein
50     ;
51     ; US-08-460-512-4

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Query Match	34.4%;	Score 418.5;	DB 1;	Length 252;
Best Local Similarity	40.0%;	Pred. No. 3.8e-32;		
Matches 104;	Conservative 46;	Mismatches 63;	Indels 47;	Gaps 9;

Db 133 SLNFEELKNLESRLKSGSRVRSKKHEMLVAIEYMOKEIETLONDNDNYLRSKITERTGL 192
 QY 173 IROENDELAK-KIYETEGSPGVNRESPTPFNFAVETRDVVOJELSTLPQONN 231
 Db 193 QOQESSVTHOGTVRES-GVTSOSHSGQYNNRYIAVNLLE-----PNOSSNDOP 241
 QY 232 PKLGILTL 239
 Db 242 P---LQLV 246

RESULT 6
 US-08-460-512-7
 ; Sequence 7, Application US/08460512
 ; Patent No. 5744693
 ; GENERAL INFORMATION:
 ; APPLICANT: MEYEROWITZ, ELIJAH M.
 ; APPLICANT: YANOFSKY, Martin F.
 ; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Richard F. Treacartin
 ; STREET: 4 Emparadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/460,512
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/293,278
 ; FILING DATE:
 ; APPLICATION NUMBER: US/07/956,694
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Treacartin, Richard F.
 ; REGISTRATION NUMBER: 31,801
 ; REFERENCE/DOCKET NUMBER: A-57322/RF
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 248 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-460-512-7

Query Match 33.7%; Score 409.5; DB 1; Length 248;
 Best Local Similarity 37.1%; Pred. No. 2.7e-31;
 Matches 93; Conservative 51; Mismatches 72; Indels 35; Gaps 6;
 QY 1 MGRGKIVIRINDSTSRQVTFKRRNGIFPKAKELATLCDAEVGLVFSSTGRLEYEST 60
 Db 17 LGRGKIEIKRIENTNNOVTFCKRRNGLKKAYELSVLCDAEVALIVFSRGRLEYEVANN 76
 QY 61 SMKSVIDRYGKA-KEEOVVANPNSELEKFMOREAASLRQOLHNIOENTYROLTGDDLSGLN 119
 Db 77 SVKATIERKKKACDSSNTGSISEANQYQOEASKLRQOIGNONNRMMLGESIALALS 136
 QY 120 VKELQSLQENOLETSLRGVAKKDHLLIDEIHLNKKASLFRQENTDLYNKNINLROENDE 179

Db 137 LRDLKNLEOKIEKISIRSKNNELLFAIEYMKR-----EIDLHN-----NNQY 182
 QY 180 LHKKIYETEGSPGVNRES-----PTPFNFAVETRDVVOJELSTLPQONN 225
 Db 183 LRKKAIEFERAQQOQQOQQOQNNMLPGSSYELVPPPHQF---DTRN---YLOVNGIQTNNH 236
 QY 226 IEPSTAPKGL 236
 Db 237 YTRQDQPSIQL 247

RESULT 7
 US-09-067-800-6
 ; Sequence 6, Application US/09067800
 ; Patent No. 6198024
 ; GENERAL INFORMATION:
 ; APPLICANT: Yanofsky, Martin F.
 ; APPLICANT: Ferrandiz, Cristina
 ; TITLE OF INVENTION: Seed Plants Characterized by Delayed
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/067,800
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-UD 2948
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 248 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-067-800-6

Query Match 33.3%; Score 405; DB 4; Length 248;
 Best Local Similarity 43.9%; Pred. No. 7.2e-31;
 Matches 90; Conservative 42; Mismatches 55; Indels 18; Gaps 5;
 QY 1 MGRGKIVIRINDSTSRQVTFKRRNGIFPKAKELATLCDAEVGLVFSSTGRLEYEST 60
 Db 16 LGRGKIEIKRIENTNNOVTFCKRRNGLKKAYELSVLCDAEVALIVFSRGRLEYEVANN 75
 QY 61 SMKSVIDRYGKAKEEOVVANPNSELEKFMOREAASLRQOLHNIOENTYROLTGDDLS 116
 Db 76 SVRGTEIRKKKACD---AVNPVSYTEANTQYQOEASKLRQOIRHDIONSNRHIVGESLG 132
 QY 117 GLNVEQLQSLQENOLETSLRGVAKKDHLLIDEIHLNKKASLFRQENTDLYNKT----- 170
 Db 133 SLNFEELKNLESRLKSGSRVRSKKHEMLVAIEYMOKEIETLONDNDNYLRSKITERTGL 192
 QY 171 NLIROENDELH-KIYETEGSPGVN 194
 Db 193 NPQOQESSVTHOGTVRES-GVTSOSHSGQYNNRYIAVNLLE-----PNOSSNDOP 241

RESULT 8

US-09-349-677-6
; Sequence 6, Application US/09349677
; Patent No. 6288305

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.
APPLICANT: Ferrandiz, Cristina
TITLE OF INVENTION: Seed Plants Characterized by Delayed
TITLE OF INVENTION: Seed Dispersal
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/349,677
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/067,800
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: Protein
US-09-349-677-6

Query Match 33.3%; Score 405; DB 4; Length 248;

Best Local Similarity 43.98; Pred. No. 7.2e-31;
Matches 90; Conservative 42; Mismatches 55; Indels 18; Gaps 5;

QY 1 MGRGIVIRIDNSTSRQVTFSEKRRNGIFKKAKELAILCDAEVGLVIFSSGRLYEYSST 60
DB 16 IGRGIEIKRIENTNRQVTFCKRRNGILKKAYELSVLCDAEVALVIFSTGRILEYANN 75
QY 61 SMKSVIDRYGAKKEQOVVNPNS---ELKFWOREASLSLROQLHNIQENYRQLTGDDLS 116
DB 76 SVRGIEIRYKACSD---AVNPSPYTEANTQYOOEASKLRQIRIDIONSNRHIVGESLG 132
QY 117 GLNVELOSLSLENOLETSRGVRAKRDHLLIDEIHDINKKASLFQOENTDLYNKI----- 170
DB 133 SLNKEKLNLGRLLEKGISRVRSKKNELVAIEYWMOKREMELOHNNYIFAKIAEGARL 192
QY 171 NLIRQENDELH-KRIYETEGPSGVN 194
DB 193 NPDOESSVIGTIVYE---SGVS 213

RESULT 9

US-08-867-087B-17
; Sequence 17, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung

TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:

ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,087B
FILING DATE: June 2, 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/323,449
FILING DATE: October 14, 1994
APPLICATION NUMBER: U.S. 08/485,981
FILING DATE: June 7, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-47071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 226-9446
INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 248 amino acid residues
TYPE: amino acid
TOPOLOGY: Linear
US-08-867-087B-17

Query Match 33.0%; Score 401; DB 2; Length 248;

Best Local Similarity 37.0%; Pred. No. 1.7e-30;
Matches 94; Conservative 50; Mismatches 74; Indels 36; Gaps 7;

QY 1 MGRGIVIRIDNSTSRQVTFSEKRRNGIFKKAKELAILCDAEVGLVIFSSGRLYEYSST 59
DB 1 MGRGIVIRIDNSTSRQVTFSEKRRNGIFKKAKELAILCDAEVGLVIFSSGRLYEYSST 60
QY 60 TMSKSVIDRYGAKKEQOVVNPNS---ELKFWOREASLSLROQLHNIQENYRQLTGDDLS 108
DB 61 QSMRTIRYKOKFSYGGPDITAIQNKENELVOSSENYL-----LKAIVENLQRTOR 112
QY 109 QLTGDDLSGLNVELOSLSLENOLETSRGVRAKRDHLLIDEIHDINKKASLFQOENTDLYN 168
DB 113 NLGDELDGTIGIELQLEKQDLSLRHIRSTQHMLOLDIQRREOMLCEANKCLRR 172
QY 169 KILIRQENDELHKKI-----YETEGPSGVNRESPTFN--FAVETRDVYQDEL 217
DB 173 KL-----EESNQLHGQVMEHATLLGYEROSPHAVQOVPHFGNGFHSLEAAEPT-LQI 227
QY 218 STLPOONNIEPSTA 231
DB 228 GFTPEOMNNSCVTA 241

RESULT 10

US-08-592-214A-4
; Sequence 4, Application US/08592214A
; Patent No. 5811536
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.

```

; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,214A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1927
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-592-214A-4

```

```

Query Match          32.3%; Score 393; DB 2; Length 253;
Best Local Similarity 35.6%; Pred. No. 1e-29;
Matches 83; Conservative 56; Mismatches 62; Indels 32; Gaps 5;

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QY 1 MGRKIVIRIDNSTSRQVFSKRRNGIFPKAKELATLIDCAEVLVIFSSGRLEYEST 60
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MGRGVQLRIENKINROVYFSKRRAGLKKAKHETSVLCDAEVALVFSHKGLFEYSTD 60
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 S-MKSVIDRYGK-AKEEQOVANPNSELEKFWOREAASLRQOLHNLQENYRLTGDDLSGL 118
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 SCMEKILERYERYSAERQLLAPESDSNTNMSMEYNRLKAKTELLERNQRYLGEDLQAM 120
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 NKELOSLLENQLETSIRGVRAKDHLLIDETIDLNKASLFHQENTDLYNKI-----NLIR 174
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 SPKEIQLNLEQOLDTALKHTRSRKQNLWDSINELQREKALQEOQNSMLSKQIKERENVLR 180
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 175 QENDELHKRIYETEGSPGVNRESPTPFNFVAVETRDVQVLESLTLPOONNIE 227
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 AAOEQWDEQNH-----GHNMPPPP-----PQOHQIQ 207

```

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RESULT 11
US-08-659-188-4
; Sequence 4, Application US/08659188
; Patent No. 6002069
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
;
; COMPUTER READABLE FORM:
;
; 9

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,188
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-659-188-4

```

```

Query Match          32.3%; Score 393; DB 3; Length 253;
Best Local Similarity 35.6%; Pred. No. 1e-29;
Matches 83; Conservative 56; Mismatches 62; Indels 32; Gaps 5;

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QY 1 MGRKIVIRIDNSTSRQVFSKRRNGIFPKAKELATLIDCAEVLVIFSSGRLEYEST 60
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MGRGVQLRIENKINROVYFSKRRAGLKKAKHETSVLCDAEVALVFSHKGLFEYSTD 60
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 S-MKSVIDRYGK-AKEEQOVANPNSELEKFWOREAASLRQOLHNLQENYRLTGDDLSGL 118
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 SCMEKILERYERYSAERQLLAPESDSNTNMSMEYNRLKAKTELLERNQRYLGEDLQAM 120
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 NKELOSLLENQLETSIRGVRAKDHLLIDETIDLNKASLFHQENTDLYNKI-----NLIR 174
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 SPKEIQLNLEQOLDTALKHTRSRKQNLWDSINELQREKALQEOQNSMLSKQIKERENVLR 180
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 175 QENDELHKRIYETEGSPGVNRESPTPFNFVAVETRDVQVLESLTLPOONNIE 227
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 AAOEQWDEQNH-----GHNMPPPP-----PQOHQIQ 207

```

```

RESULT 12
US-08-655-227-4
; Sequence 4, Application US/08655227
; Patent No. 6025483
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Maize and Cauliflower APETALAI Gene
; TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,227
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815

```



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Db      1  MGRGRVQJAKRIENKINPOVTFKRRAGLMMKKAHEISVLCDAEVALVPSHKGILFEYSTD 60
QY      61  S-MKSVIDRYGK-AKEEOVVANPNSELKFWOREASLRQOLHNIQENYRQLTGDDLSGL 118
Db      61  SCMEKILEYERYSYAEEROLAPESDSNTNMSMEYNRKAKIETELERNQRYHLEGEDLOAM 120
QY      119 NVKEIQLSENOLETSLRGVRAKKDHLIDETIDLNKRAKSLFHOENTDLYNKI---NLIR 174
Db      121 SPKEIQLNEQQLDTALKHTRSKRNQMLYDSINELORKKAKIOLQNSMLSKQIKERENVLR 180
QY      175 QENDELHKKIYETEGSPGVNRESPTPENFAVETRDVPVQLELSTLPQONNIE 227
Db      181 AOEQOWDEQNH-----GHNMPPPP-----POOHIO 207

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RESULT 15
US-09-398-326-4
; Sequence 4, Application US/09398326
; Patent No. 6355863

GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
NUMBER OF SEQUENCES: 26
REPRODUCTIVE Development and Methods of Making Same

CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,326

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/659,188

FILING DATE: 05-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 3739

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 253 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-398-326-4

Query Match 32.38; Score 393; DB 4; Length 253;

Best Local Similarity 35.68; Pred. No. 1e-29;

Matches 83; Conservative 56; Mismatches 62; Indels 32; Gaps 5;

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QY      1  MGRKIVIRIDNSTSRQVFSKRRNGIFPKAKELATIDCAEGLVYFSSGRLEYEST 60
Db      1  MGRGRVQJAKRIENKINPOVTFKRRAGLMMKKAHEISVLCDAEVALVPSHKGILFEYSTD 60
QY      61  S-MKSVIDRYGK-AKEEOVVANPNSELKFWOREASLRQOLHNIQENYRQLTGDDLSGL 118
Db      61  SCMEKILEYERYSYAEEROLAPESDSNTNMSMEYNRKAKIETELERNQRYHLEGEDLOAM 120
QY      119 NVKEIQLSENOLETSLRGVRAKKDHLIDETIDLNKRAKSLFHOENTDLYNKI---NLIR 174

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Db      121 SPKEIQLNEQQLDTALKHTRSKRNQMLYDSINELORKKAKIOLQNSMLSKQIKERENVLR 180
QY      175 QENDELHKKIYETEGSPGVNRESPTPENFAVETRDVPVQLELSTLPQONNIE 227
Db      181 AOEQOWDEQNH-----GHNMPPPP-----POOHIO 207

```

Search completed: August 11, 2002, 09:36:43
Job time: 3498 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 11, 2002, 08:42:20 ; Search time 43.45 Seconds

(without alignments)
530.758 Million cell updates/sec

Title: US-09-970-624-2

Perfect score: 1216
Sequence: 1 MGRGKIVIRIDNSTSRQVT.....PQNNIEPSTAPKLGILIP 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_71.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	729.5	60.0	234	2	T17029
2	666	54.8	228	2	T05621
3	643.5	52.9	227	2	H84614
4	638.5	52.5	234	2	T52100
5	636.5	52.3	234	2	A84515
6	605	49.8	240	2	T09700
7	589	48.4	239	2	T45801
8	435	35.8	261	2	S51935
9	428.5	35.2	222	2	S51934
10	426.5	35.1	284	2	T05033
11	426.5	35.1	284	2	A85214
12	425	35.0	261	2	T09603
13	420	34.5	262	2	T08039
14	419.5	34.5	230	2	T04000
15	418.5	34.4	252	2	A43484
16	417.5	34.3	242	2	J02212
17	417	34.3	246	2	E39534
18	416	34.2	229	2	T08040
19	414	34.0	258	2	G84858
20	409.5	33.7	248	2	T03592
21	408.5	33.6	248	2	T07185
22	405	33.3	248	2	A39534
23	405	33.3	254	2	T10185
24	403	33.1	265	2	T02261
25	402.5	33.1	236	2	S59480
26	402.5	33.1	242	2	T10486
27	402.5	33.1	242	2	T09571
28	401	33.0	248	2	T04170
29	401	33.0	257	2	S53306

30	401	33.0	259	2	T01700
31	399.5	32.9	248	2	S20886
32	394.5	32.4	250	2	T04167
33	393	32.3	246	2	T17023
34	392	32.2	286	2	J02289
35	391.5	32.2	239	2	A44543
36	390.5	32.1	242	2	S71208
37	390	32.1	247	2	S60307
38	386.5	31.8	227	2	S23730
39	385.5	31.7	254	2	S52236
40	385	31.7	253	2	S57586
41	385	31.7	273	2	T03410
42	384	31.6	250	2	T07100
43	383.5	31.5	225	2	T04168
44	383	31.5	256	2	S27109
45	381.5	31.4	219	2	S46526

ALIGNMENTS

```

RESULT 1
T17029
MADS-box transcription factor DEFH125 - garden snapdragon
C:Species: Antirrhinum majus (garden snapdragon)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T17029
R:Zachgo, S.; Saedler, H.; Schwarz-Sommer, Z.
Plant J. 11, 1043-50, 1997
A:Title: Pollen-specific expression of DEFH125, a MADS-box transcription factor in An
A:Reference number: Z14458; MUID:9193074
A:Accession: T17029
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-234 <ZAC>
A:Cross-references: EMBL:Y10750
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho
C:Keywords: transcription factor

Query Match 60.0%; Score 729.5; DB 2; Length 234;
Best Local Similarity 63.2%; Pred. NO. 1.5e-42;
Matches 146; Conservative 32; Mismatches 52; Indels 1; Gaps 1;

QY 1 MGRGKIVIRIDNSTSRQVTFSKRRNGIFKKAKELATLCOAEVGLYFSSGRLYESST 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGRGKIVIRIDNSTSRQVTFSKRRSGILKKAKELATLCOAEVGLYFSSGRLYESST 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SMKSVIDRYGKAKERQGVANPNSELKFWQREASLRQQLHNLQENYROLTGDDLSGLNV 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SMKSTIERHTKTKEDHOLLHNGSVKFWQREAAITLRQQLDLENHRLKLGELQGLNV 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 KELOSLENQLETSKGVARAKDHLIDEIIDLNRKASLFHOENFDLTKMLIQEDEL 180
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 EDIHLLENQLEMSLGVAKKVKOMLTDEVHLRRKGCHLHQENNELYEKVLLOQENKEL 180
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 161 HKKITETGSPGSVNRSPENPAVETRDVQVLELSTPQNNIEPSTA 231
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 161 CKAAGTQDVSAANGTALVPFGALGRQFPFIQLHLSQ-PEPENIETSTRA 230
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
T05621
MADS-box protein AGL17 homolog F20D10.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-Aug-1999
R:Bayan, M.; Medler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer,
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15420
A:Accession: T05621
A:Molecule type: DNA
A:Residues: 1-228 <BEV>

```


QY	2	GKGIVIRRIDNSTROYTFESKRRRGIFKKAELALICDAEGLVTFESTGTYEYSS	61
		: : : : : : : : :	
Db	50	GKGKIEIKRIENTNTKQVYFCRRRGLLKAELSVLCOAEVALLVSSRGKLYEYSNS	109
QY	62	MKSVIDRYGAKEEQO---VYANPSELKFWOREAASLRQULHNIOENYRQLTGDDLGL	118
		: : : : : : : : : : :	
Db	110	YKGTIEREKKALSDMSNTGSAVEINAQ---YYQOESAKLMOQLITISONSRLMGFTIGSM	167
QY	119	NKYELOSLENQETSLRQVRAKKDHLIDETHDLNRKASLTFQEWNTDLYNKLNLRQEND	178
		: : : : : : : : : : : :	
Db	168	SPKELRNIEGRERSITRIRSKKNELLFSEIDYMKRREVDLNDMOILAKI---AEME	223
QY	179	ELHKRIYETEGPSGVNRRESPTPFNFVAVETRDVPVO---LELSTLPQOONNTEPSTA	231
		: : : : : : : : : : :	
Db	224	RNNPSTISLMPGGSNYEQMLMPD-----QTOSQPDPSRNYFQVALV-QPNNHHSASAGNQ	276
QY	232	PKLGLOLI 239	
		: : : : : : : : : : : :	
Db	277	DOTALQLV 284	

RESULT 12

T09603

MADS-box protein 3 - Monterey pine

C;Species: Pinus radiata (Monterey pine)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000

C;Accession: T09603

R;Mouradov, A.; Loopsira, C.; Southern, S.; Glassick, T.; Marshal, H.; Teasdale, R. submitted to the EMBL Data Library, October 1996

A;Accession: T09603

A;Reference number: 216765

A;Status: preliminary; translated from GR/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-261 <MOU>

A;Cross-references: EMBL:U76726; NID:g2160700; PID:g2160701

A;Experimental source: tissue-type Immature male and female cones

C;Genetics:

A;Gene: MADS3

C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homology

C;Keywords: DNA binding; transcription regulation

P;2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match	35.0%	Score 425;	DB 2;	Length 261;
Best Local Similarity	40.8%;	Pred. No. 7.7e-22;		
Matches	89;	Conservative	44;	Mismatches 61; Indels 24; Gaps 4;
QY	1	MGRGAVIRIRIDINSNSROYTFESKRNRNGJFFKKAKELAILCDADAVGVITFESSTGLYEYSST	60	
DB	1	MGRGVOLFRRIENKINROYTFESKRNRNGLLKAYELSYLDCADAVALLIFSTRKLEFFASS	60	
QY	61	SNKSVSDIRYGRKK-EEQQVYANPNSELKFWQEEAASLRQOLHNLDENRQTLTGDDLSGIN	119	
DB	61	SNKTLIEREKSSVAMQDTTGVSDREDAONHMEVTKLKGVELLDRSORHLLGEBIDGPIIN	120	
QY	120	VKELOSLNQELTSLRGVYAKDKHLILDEIHLNKRKASLFEHOENTDLYKINILIRQENDE	179	
DB	121	VKELOQLERQLEVALTHLRSKRTQYMDQIEBLRQRERLH-----EVNKS	166	
QY	160	LHKRTYETGCP---SGVNRRESPT-----PPIFAVYET	208	
DB	167	LQKRLSTEGRDVITGIEQTSNTNTGTNGPMDSSITNT	204	

RESULT 13
T08039
MADS-box protein - cucumber
C.Species: Cucumis sativus (Cucumber)
C.Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C.Accession: T08039
R.Kater, M.M.; Colombo, L.; Franken, J.; Busscher, M.; Masiero, S.; van Lookeren Campagne
Plant Cell 10, 171-182, 1998

A>Title: Multiple AGAMOUS homologs from cucumber and petunia differ in their ability
A.Reference number: Z16308; MUID:98156685
A.Accession: T08039
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-262 <KAT>
A.Cross-references: EMBL:AF035438; NID:g2997612; PIDN:AAC08528.1; PID:g2997613
C.Genetics:
A.Gene: CUM1
C.Superfamily: transcription factor squa; serum response factor DNA-binding domain ho
C.Keywords: DNA binding; nucleus; transcription regulation
F743-98/Domain: serum response factor DNA-binding domain homology <SRF>

```

Query Match Similarity      34.5% : Pred No. 1.7e-21;
Best Local Similarity      39.8% : Pred No. 1.7e-21;
Matches       96; Conservative    47; Mismatches     76; Indels   22; Gaps      5;

QY      1 MGGRKIVIRRIDNSTSROYTFSKRRNGIFPKAKELAILCDAEVLGVFSSSTGLYEYSST 60
          ||||| :||| :||| ||||| ||||| :||| ||||| :||| ||||| :|||
Db       42 MGRGKEIKRIINTNTNROYTFCFKRRGLTKKKRYEVLCDAAVALVLFSSRGLLEYAANN 101
          ||||| :||| ||| :||| :||| :||| :||| :||| :||| :||| :|||
QY      61 SAKSVIDRYGRKAEEQOYYVANPN-SELTKWOREAKSLROOLNLIOENVQLQGDDLSGN 119
          |::| :||| ||| :||| :||| :||| :||| :||| :||| :||| :|||
Db       102 SYKATLIDRKKKASSDSSSNSTSGTSSEANTORYQOEBAKLRLQIENGLONSNNMIGESISLT 161
          ||||| :||| ||| :||| :||| :||| :||| :||| :||| :||| :|||
QY      120 VKELOLENOLETSLRGVARAKKDHLIDEIHDLNRKASLFHQENTDLYKNILNQENDE 179
          ||||| :||| :||| :||| ||||| ||||| :||| ||||| :||| |||||
Db       162 AADLDGLEETFEKTEKGISIRISKNNELLFAELEVMYRRK-----EIDLHNNNMOMLRKIAIE 214
          ||||| :||| :||| :||| ||||| ||||| :||| ||||| :||| |||||
QY      180 LAKKIYETFGPSGVNRESRP-TPEFNVAVVTRDPVPOLELSTLPPOONNIIEPTAPRKLGLOL 238
          ||||| :||| :||| :||| ||||| ||||| :||| ||||| :||| |||||
Db       215 SERNNVMMMGCEFIQLQSHYPDPRDFQVYGLOHNHO-----YPRQDN-----MALQL 261
          ||||| :||| :||| :||| ||||| ||||| :||| ||||| :||| |||||
QY      239 I 239
          :
Db       262 V 262

```

```

RESULT 14
T04000
MADS-box protein AGL1 - Arabidopsis thaliana
N:Alternate names: protein T5L19.90
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999
C:Accession: T04000
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15184
A:Accession: T04000
A:Molecule type: DNA
A:Residues: 1-230 <BEV>
A:Cross-references: EMBL:AL049481
A:Experimental source: cultivar Columbia; BAC clone T5L19
C:Genetics:
A:Gene: AGL1
A:Map position: 4
A:Introns: 61/2; 88/3; 109/2; 142/3; 156/3; 170/3
A:Note: T5L19.90
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain
C:Keywords: DNA binding
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

```

Query Match	34.5%	Score	419.5	DB.2	Length	230:	
Best Local Similarity	45.0%	Pred. No.	1,5e-21:				
Matches	86	Conservative	42:	Mismatches	56:	Gaps	2:
				Indels	5:		
QY	1	MGRKATVIRPRDINSTSROYTFPSKRNGIFPKKKELAILDCAEGLVINSSTRLEYSSST	60				
DB	1	MGRGATIEKRIENSTNRQVTECFRRRGLKKKELSYLDCDAEVALIVFSTRLEYAANN	60				
QY	61	SMKSVADRYGAKKEQ--QVYANPNPNSIKAFQREAAALRQGLAHNIOENRYRLTSDDDLSC	117				

Db	61	NRSTIEYKKACDSTNTSTVQEIINA - AYVQGEASIKRQIQITQINRNRLMDGSLSS	118
Qy	118	LNVEKLESLNQLSTLRGVAKKDHLLIDELHDLNRKSLSPHOENTLYNKINILRQEN	177
Db	119	LSVELKQVEERLEKATSRIRSKKHELLIVEINMAOKREIELDNENIYLRTVAEAEVRYQ	178
Qy	178	DELHKKIYEFY	188
Db	179	QHHHQMVSGET	189

RESULT 15

probable transcription factor BAG1 - rape
C:Species: Brassica napus (rape)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
C:Accession: A43484
R:Mandel, M.A.; Bowman, J.L.; Kempin, S.A.; Ma, H.; Meyerowitz, E.M.; Yanofsky, M.F.
Cell 71, 133-143, 1992
A:Title: Manipulation of flower structure in transgenic tobacco.
A:Reference number: A43484; MUID:93008236
A:Accession: A43484
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-252 <MAN>
A:Cross-references: GH:M59415; NID:g167125; PIDN:AAA32985.1; PID:g167126
A:Note: sequence extracted from NCBI backbone (NCBI:P.115468)
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homo
C:Keywords: DNA binding; nucleus; transcription regulation
C:ID-73/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match	34.4%	Score 418.5	DB 2	Length 252
Best Local Similarity	40.0%	Pred. No. 2e-21		
Matches	104	Conservative	46	Mismatches 63
				Indels 47
				Gaps 9
QY	2	CGGKTVIRIDNSTSRQVTFKRRMGIEFKAKELALICDAEVLVFSSTGRLEYESSVS	61	
Db	18	CGKTEIKKIEITNTNROYTFCKRRNGLLKAKVELSLVLCDAEVALVFSRGRLEYSSNS	77	
QY	62	MKSVDRYGRKAKEEO--VVANPNSLKFQWREASLQOOLHNLOENRQTLGGDSL	118	
Db	78	VAGTIERKKALSDNSNNGVAELNAQ--YYQGESKTLRQOILISIQNSRKRLMGELISGM	135	
QY	119	NKVELQSLLENQLETSLRGYRRAKDHLLDEIHDLNKASLPHQENTDLYNKINLLROEND	178	
Db	136	SEKRELRNLEGRIDRSVNRIRSKNELLFAEIDYMKR-----EVDLHN-----DNQ	181	
QY	179	ELHKKIYETEG-----PSCVNRN-----SPTPEFAVVEETRDVPVQLELSTLQ	222	
Db	182	LLRAKIAERERNNPPMSLMPGGSNNLEQIMPPQTOGPQF-----DSRRNFQVVAL-Q	232	
QY	223	QNNIEPSTA---PKLGLQLI	239	
Db	233	PNNHHYSAGREDQATALQV	252	

Search completed: August 11, 2002, 09:37:47
Job time: 3327 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 11, 2002, 09:36:49 ; Search time 24.99 Seconds
(without alignments)
371.856 Million cell updates/sec

Title: US-09-970-624-2

Perfect score: 1216
Sequence: 1 MGSKIVIRINDNSTROYT.....POONIEPSTAPKLGILIP 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	666	54.8	228 1	AG1Y_ARATH Q982J6 arabidopsis
2	643.5	52.9	227 1	AG17_ARATH Q38840 arabidopsis
3	426.5	35.1	252 1	AG_ARATH P17839 arabidopsis
4	419.5	34.5	230 1	AG1L_ARATH Q38836 arabidopsis
5	418.5	34.4	252 1	AG_BRANA Q01540 brassica na
6	417.5	34.3	242 1	AG_PETHY Q40885 petunia hyb
7	417	34.3	246 1	AG1S_ARATH P29385 arabidopsis
8	414.5	34.1	242 1	AG_PANGI Q40872 panax gins
9	409.5	33.7	248 1	AG_TOBAC Q45885 nicotiana t
10	408.5	33.6	248 1	AG_LYCES Q40168 lycopersico
11	405	33.3	248 1	AG1L_ARATH P29381 arabidopsis
12	390.5	32.1	242 1	AG1L_ARATH Q38876 arabidopsis
13	389.5	32.0	221 1	AG1L_SINAP Q41274 sinapis alb
14	386.5	31.8	227 1	AG1L_LYCES Q40170 lycopersico
15	386	31.7	265 1	Q91UY6 lycopersico
16	385.5	31.7	254 1	JOIN_LYCES Q41276 sinapis alb
17	384	31.6	250 1	AG1L_SOLTU Q42429 solanum tub
18	383.5	31.5	255 1	AG1L_ARATH P35631 arabidopsis
19	380	31.2	240 1	AG1L_ARATH Q91YCI arabidopsis
20	378	31.1	250 1	AG1L_SOLCO Q23228 solanum com
21	375	30.8	248 1	AG1L_ARATH P29382 arabidopsis
22	373.5	30.7	252 1	AG1L_ARATH P29386 arabidopsis
23	373	30.7	233 1	CMR1_DIACA Q39685 dianthus ca
24	372.5	30.6	268 1	AG1S_ARATH Q38847 arabidopsis
25	372	30.6	241 1	AG1L_PETHY Q03489 petunia hyb
26	365	30.0	250 1	AG1L_ARATH P29384 arabidopsis
27	364.5	29.9	244 1	AG13_ARATH Q38837 arabidopsis
28	363	29.9	214 1	SOCI_ARATH Q6445 arabidopsis
29	357	29.4	224 1	AG19_LYCES Q42464 lycopersico
30	354	29.1	219 1	AG19_ARATH Q82743 arabidopsis
31	354	29.1	258 1	AG13_ARATH P29383 arabidopsis
32	353.5	29.1	251 1	AG19_ARATH P29385 arabidopsis
33	350.5	28.8	264 1	AG1S_BRANA Q39295 brassica na

34	349.5	28.7	254 1	AG19_SINAP Q04067 sinapis alb
35	346.5	28.5	250 1	AG1L_ARADE Q38694 aranda debo
36	337.5	27.7	209 1	GLOB_TOBAC Q03416 nicotiana t
37	336.5	27.7	221 1	AG14_ARATH Q38838 arabidopsis
38	335	27.5	210 1	FBP1_PETHY Q03488 petunia hyb
39	307.5	25.3	215 1	GLOB_ANTMA Q03478 antirrhium
40	307	25.2	212 1	MAD2_PETHY Q07474 petunia hyb
41	306	25.2	211 1	AG12_ARATH Q38841 arabidopsis
42	303	24.9	231 1	MAD1_PETHY Q07472 petunia hyb
43	297	24.4	214 1	CMR2_DIACA Q42498 dianthus ca
44	296	24.3	196 1	FLC_ARATH Q95797 arabidopsis
45	289.5	23.8	232 1	AP3_ARATH P35632 arabidopsis

ALIGNMENTS

RESULT 1	AG1Y_ARATH	STANDARD:	PRT:	228 AA.
AC	Q982J6	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Agamous-Like MADS box protein At4g37940.			
GN	AT4G37940 OR F20D10.60.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:			
OC	Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:			
OC	eurosid II: Brassicales: Brassicaceae: Arabidopsis.			
OX	NCBI_Taxid=3702:			
RM	[1]			
RP	SEQUENCE FROM N. A.			
RC	STRAIN=CV. COLDWATER:			
RX	MEDLINE=20083488: Pubmed=10617198:			
RA	Mayer K.F.X., Schueler C., Wambutt R., Murphy G., Volkhaert G.,			
RA	Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,			
RA	Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,			
RA	Weichselgartner M., de Simone V., Obermaier B., Macho R., Mueller M.,			
RA	Kreis M., Deiseny M., Puigdomenech P., Watson M., Schmidheini T.,			
RA	Reichert B., Portelle D., Perez-Alonso M., Bourtay M., Bancroft I.,			
RA	Vos P., Hohelsel J., Zimmermann W., Weller H., Riddle P.,			
RA	Langham S.-A., McCullagh B., Bilham L., Robben J.,			
RA	Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandebussche F.,			
RA	Breken M., Welfens I., Voet M., Bastiaens I., Aert R., Defoor E.,			
RA	Wetzellegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,			
RA	Holzer E., Brandt A., Peters S., van Stavelen M., Dirkse W.,			
RA	Moolijman P., Klein Lankhorst R., Rose M., Haut J., Koether P.,			
RA	Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,			
RA	De Keyser A., Buysschaert C., Gielen J., Villarroel R., De Clercq R.,			
RA	Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,			
RA	Clark L., Doggett J., Hall S., Kay M., Leonard N., McIay K., Mayes R.,			
RA	Petelt A., Rajendram M.A., Lyne M., Benes V., Reichtmann S.,			
RA	Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,			
RA	Gabel S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,			
RA	Dose C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzel A.,			
RA	Neumann S., Argitaley A., Vitale D., Liqouri R., Piravandi E.,			
RA	Massenet O., Quigley F., Clabaud G., Mwendlein A., Felber R.,			
RA	Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,			
RA	Chedror F., Cooke R., Berger C., Monfort A., Cascuberta E.,			
RA	Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,			
RA	Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,			
RA	Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bleske C.,			
RA	Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,			
RA	Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Hebermann K.,			
RA	Parrell L., Dedha N., Gnoj L., Schutz K., Huang E., Spiegel L.,			
RA	Sekon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,			
RA	Stokem T., Kalicki J., Graves T., Hamon G., Edwards J.,			
RA	Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,			
RA	Mix P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,			
RA	Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,			
RA	Nelson J., Speth J., Ryan E., Andrews S., Geisel C., Layman D.,			
RA	Du H., Ali J., Bernhoff A., Jones K., Drone K., Cotton M., Joshi C.,			

RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekhar M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
 RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lohi M., Johnson A.,
 RA Chen E., Marra M., Marienssens R., McCombie W.R.,
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:769-777(1999).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
 CC -----
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 CC -----
 DR EMBL: AL035538; CAB37534.1; -;
 DR EMBL: AL161592; CAB80459.1; -;
 DR HSSP: P11831; ISRS.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 KM Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3 57 MADS.
 FT DOMAIN 95 167 K-BOX.
 FT SEQUENCE 228 AA; 26411 MW; 87077BFB6CC4F7A6 CRC64;

Query Match 54.8%; Score 666; DB 1; Length 228;
 Best Local Similarity 59.0%; Pred. No. 2, 2e-37;
 Matches 138; Conservative 36; Mismatches 50; Indels 10; Gaps 3;

QY 1 MGRGKIVIRIDNSTSQVTFSSKRRNGIFKKAKELATLCAEVLGYFFSSGRLYEYSST 60
 DB 1 MGRGKIVIRIDNSTSQVTFSSKRRNGIFKKAKELATLCAEVLGYFFSSGRLYEYSST 60
 QY 61 SMKSVIDRYGKAKEEQVAVNPNSLKFQWRKASLRQQLHNLQENTROLTGDDLSGLNV 120
 DB 61 SMKSVIDRYGKAKEEQVAVNPNSLKFQWRKASLRQQLHNLQENTROLTGDDLSGLNV 120
 QY 121 KELOSLENOLETSLRGVAKKDHLLIDEIHLNKKASLFFQENTDLYNKINLIRQENDEL 180
 DB 121 KELOSLENOLETSLRGVAKKDHLLIDEIHLNKKASLFFQENTDLYNKINLIRQENDEL 180
 QY 121 NEUNSLJENQLEISLRGIRMKKEQLLTQEIOLSKRLIHQEWLDSKRYQRTHQENVEL 180
 DB 121 NEUNSLJENQLEISLRGIRMKKEQLLTQEIOLSKRLIHQEWLDSKRYQRTHQENVEL 180
 QY 181 HKKITYEGSGVNRSPPTPNFAVETRD-VPVQLELSTLPQOONIEPSTAPK 233
 DB 181 HKKITYEGSGVNRSPPTPNFAVETRD-VPVQLELSTLPQOONIEPSTAPK 233
 DB 181 YKRAYMANTNGFTHRE-----VAVADDESHQIRLOLS---QPEHSDYDTPPR 225

RESULT 2
 AG17_ARATH STANDARD; PRT; 227 AA.
 AC Q3840; Q92050;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Agamous-like MADS box protein AG17.
 GN AG17 OR At2g22630 OR T9122.7.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucoside II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLOMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Honning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE OF 8-227 FROM N.A.
 RC STRAIN=CV. LANDSBERG. ERCTA; TISSUE=ROOT;
 RX MEDLINE=96004530; PubMed=7549482;
 RA Rounsley S.D., Ditta G.S., Yanofsky M.F.;
 RL Plant Cell 7:1259-1269(1995).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: PREPARENTALLY EXPRESSED IN ROOTS.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -----
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 CC -----
 DR EMBL: AC006340; AAD15571.1; -;
 DR EMBL: U20186; AAC49084.1; -;
 DR HSSP: P11746; INNM.
 DR TRANSFAC: T03020; -;
 DR Mendel: 6456; Arabid; MADS; 6456.
 DR Mendel: 39770; Arabid; MADS; 39770.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 2.
 KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3 57 MADS.
 FT DOMAIN 95 167 K-BOX.
 FT CONFLICT 201 227 AYESHAQVRLQSLQPEQSHYKTSNS -> QENPMHRLG
 FT CS (IN REF. 2).
 FT SEQUENCE 227 AA; 26314 MW; 2C02283974D76594 CRC64;

Query Match 52.9%; Score 643.5; DB 1; Length 227;
 Best Local Similarity 57.0%; Pred. No. 6, 5e-36;
 Matches 131; Conservative 46; Mismatches 48; Indels 5; Gaps 3;

QY 1 MGRGKIVIRIDNSTSQVTFSSKRRNGIFKKAKELATLCAEVLGYFFSSGRLYEYSST 60
 DB 1 MGRGKIVIRIDNSTSQVTFSSKRRNGIFKKAKELATLCAEVLGYFFSSGRLYEYSST 60
 QY 61 SMKSVIDRYGKAKEEQVAVNPNSLKFQWRKASLRQQLHNLQENTROLTGDDLSGLNV 120
 DB 61 SMKSVIDRYGKAKEEQVAVNPNSLKFQWRKASLRQQLHNLQENTROLTGDDLSGLNV 120
 QY 121 KELOSLENOLETSLRGVAKKDHLLIDEIHLNKKASLFFQENTDLYNKINLIRQENDEL 180
 DB 121 KELOSLENOLETSLRGVAKKDHLLIDEIHLNKKASLFFQENTDLYNKINLIRQENDEL 180

Db 121 KELLONISQLEMSLDRGIRMRQELTNEIKELTRKRLVHHEMLLSRKVQRIHOENVEL 180
 QY 181 HKRIYEEGSGVNRSPFPNFVETRPVQLELSTIPQOONIEPST 230
 Db 181 YKRAYGTSNTGILGHELDV--AVYESH-AQVRLQLSQ-PEQSHYKTS 225

RESULT 3
 AG_ATH ID AG_ATH STANDARD; PRT; 252 AA.

AC P17839;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE AGAMOUS protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;

SEQUENCE FROM N.A.
 RC STRAIN-CV. LANDSBERG. ERECTA;
 RX MEDLINE=9030968; PubMed=1973265;
 RA Yanofsky M.F., Ma H., Bowman J.L., Drews G., Feldmann K.A.,
 RA Meyerowitz E.M.;
 RT "The protein encoded by the Arabidopsis homeotic gene agamous
 RT resembles transcription factors.";
 RL Nature 346:35-39(1990).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
 CC GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
 CC FLOWERS.

CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- MISCELLANEOUS: MUTATIONS IN THE AG GENE RESULT IN THE REPLACEMENT
 CC OF THE SIX STAMENS BY SIX PETALS AND OF THE CARPELS BY A NEW
 CC FLOWER.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).

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DR EMBL: X53579; CA37642.1; ALT_INT.
 DR PIR: S10933; S10933.
 DR HSSP: P11746; INNM.
 DR TRANSFAC: T01007;
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF00446; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS00066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Activator; Nuclear protein.
 FT DOMAIN 19 73 MADS.
 FT DOMAIN 112 184 K-BOX.
 FT CONFLICT 1 1 M->T (IN REF. 1).
 SQ SEQUENCE 252 AA; 28723 MW; 4E7591AD85654C1C CRC64;

Query Match 35.18; Score 426.5; DB 1; Length 252;
 Best Local Similarity 41.18; Pred. No. 1.4e-21;
 Matches 102; Conservative 49; Mismatches 74; Indels 23; Gaps 7;

QY 2 GKKIVIRRIDNSTSPQYFSSRRNRGIFAKKELAILDDEAGLVIFSSGTREYSSTS 61
 Db 18 GKKIKIRIEMTNTNQVFCRRNGLKKAYELSVLQDAEALLVFSRRGLYEYSNNS 77
 QY 62 MMSVIDRYKAKEEEO---VANPSELKFWOREASLRLQHLNQENTROLTGDDLSL 118
 Db 78 VKGTIERYKKAISDNGTSGVAEINQO--YQOESAKLFOQITISIONSROLMGETISM 135
 QY 119 NVKELQSLNQLSTLRGVRRAKDHLLIDEHDLNRKASLFEQEMDLYNKINLREND 178
 Db 136 SPKEILNLGRLERSTIRSKNLELSEIDYMQREYDLHNDQILRAKT---AENE 191
 QY 179 ELHKRIYETEGSGVNRSPFPNFVETRPVQ---LELSTIPQOONIEPSTA--- 231
 Db 192 RNNPSTSLMPGGSNYRLQMLPP-----QTOSOPDPSRYFQVAL-QPNNHYSAGNQ 244
 QY 232 PKLGQLI 239
 Db 245 DQTAQLV 252

RESULT 4
 AG_ATH ID AG_ATH STANDARD; PRT; 230 AA.

AC 038836;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Agamous-like MADS box protein AG11.
 GN AG11 OR AT4G09960 OR T5L19.90.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;

SEQUENCE FROM N.A.
 RC STRAIN-CV. LANDSBERG. ERECTA; TISSUE=flower;
 RX MEDLINE=96004530; PubMed=7549482;
 RT Rounsley S.D., Ditta G.S., Yanofsky M.F.;
 RT Diverse roles for MADS box genes in Arabidopsis development.";
 RL Plant Cell 7:1259-1269(1995).

RC SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wandut R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
 RA Harris B., Ansgore W., Brandt P., Griwall L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Oberwälder B., Macho R., Mueller M.,
 RA Kreis M., Dalseny M., Puigdomenech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohnel J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Billham L., Robben J.,
 RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weizengger T., Bothé G., Ramsperger U., Hilbert H., Bruun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren S., Dirse W.,
 RA Woolfman P., Klein Lankhorst R., Rose M., Hauf J., Koetler P.,
 RA Bernaisser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA de Keyser A., Buyschaert C., Gielen J., Villartiel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Leonard N., McIay K., Mayes R.,
 RA Petzelt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehnert T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Faltmann B., Grandeth K., Dauner D., Herzl A.,
 RA Neumann S., Argitlou A., Vitale D., Iguori R., Piravandi E.,
 RA Messenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lechanny A., Aubourg S.,
 RA Chefor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,

RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances S., Stocker S.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Strocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kallio J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Clout J., Abbott A., Scott K., Johnson D.,
 RA Mox P., Bentley D., Fulton B., Miller M., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante N., Pepin K., Miller L.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Giesel C., Layman D.,
 RA Du H., All J., Bergthoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekhar M., Matero A., Shah R.,
 RA Swaby I.R., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Iochi M., Johnson A.,
 RA Chen E., Marra M., Martienssen R., McCombie W.R.,
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:769-777(1999).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.

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CC -----
 DR EMBL: U20182; AAC49080.1; -;
 DR EMBL: AL049481; CAB39620.1; -;
 DR EMBL: AL161516; CAB78119.1; -;
 DR HSSP: P11746; INNM.
 DR TRANSFAC: T03009; -;
 DR Mendel: 6452; Arabid; MADS; 6452.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3 57 MADS.
 FT DOMAIN 96 168 K-BOX.
 SQ SEQUENCE 230 AA; 26183 MW; 336C383355E6CB51 CRC64;

Query Match 34.5%; Score 419.5; DB 1; Length 230;
 Best Local Similarity 45.0%; Pred. No. 3.5e-21;
 Matches 86; Conservative 42; Mismatches 58; Indels 5; Gaps 2;

QY 1 MGKGIKIRIRIDNSTRGVTFKRRNGIFKKAKELALICDAEGLVIFSSGRLEYESTS 60
 DB 1 MGKGIKIRIRIDNSTRGVTFKRRNGIFKKAKELALICDAEGLVIFSSGRLEYESTS 60
 QY 61 MGSVIDRYKRAKEEQ--OVANPNSELKFWQREASLRQQLHNIQENYROLTGDDLSG 117
 DB 61 MGSVIDRYKRAKEEQ--OVANPNSELKFWQREASLRQQLHNIQENYROLTGDDLSG 117
 QY 118 LNKELQSLQENQLETSIRGVARRKDDHLIDETHDLNRKASLPHQENTDLYNKINLRQEN 177
 DB 118 LNKELQSLQENQLETSIRGVARRKDDHLIDETHDLNRKASLPHQENTDLYNKINLRQEN 177
 QY 119 LSKVELKQVNRLEKAIKSRKSKHLLVEIENAKRTEIDENIYLRKVAEVERQ 178
 DB 119 LSKVELKQVNRLEKAIKSRKSKHLLVEIENAKRTEIDENIYLRKVAEVERQ 178
 QY 178 DELHKIYETE 188
 DB 179 QHHHOMVSGSE 189

RESULT 5
 AG-BRANA STANDARD: PRT; 252 AA.
 ID AG-BRANA
 AC Q01540;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE AGAMOUS protein.
 GN Agl.
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. WESTAR;
 RX MEDLINE=93008236; PubMed=1356631;
 RA Mandel M.A., Bowman J.L., Kemplin S.A., Ma H., Meyerowitz E.M.,
 RA Yanofsky M.F.;
 RT "Manipulation of flower structure in transgenic tobacco."
 RL Cell 71:133-143(1992).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
 CC GENES THAT DETERMINE STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
 CC FLOWERS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRP-TYPE TRANSCRIPTION FACTORS (K-BOX).

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CC -----
 DR EMBL: M99415; AAA32985.1; -;
 DR PIR: A43484; A43484.
 DR HSSP: P11746; INNM.
 DR TRANSFAC: T01773; -;
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Activator; Nuclear protein.
 FT DOMAIN 19 73 MADS.
 FT DOMAIN 112 184 K-BOX.
 SQ SEQUENCE 252 AA; 28778 MW; 7C1EF7C96C19EACE CRC64;

Query Match 34.4%; Score 418.5; DB 1; Length 252;
 Best Local Similarity 40.0%; Pred. No. 4.5e-21;
 Matches 104; Conservative 46; Mismatches 63; Indels 47; Gaps 9;

QY 2 MGKGIKIRIRIDNSTRGVTFKRRNGIFKKAKELALICDAEGLVIFSSGRLEYESTS 61
 DB 18 MGKGIKIRIRIDNSTRGVTFKRRNGIFKKAKELALICDAEGLVIFSSGRLEYESTS 77
 QY 62 MGSVIDRYKRAKEEQ--OVANPNSELKFWQREASLRQQLHNIQENYROLTGDDLSG 118
 DB 78 MGSVIDRYKRAKEEQ--OVANPNSELKFWQREASLRQQLHNIQENYROLTGDDLSG 135
 QY 119 LNKELQSLQENQLETSIRGVARRKDDHLIDETHDLNRKASLPHQENTDLYNKINLRQEN 178
 DB 136 LNKELQSLQENQLETSIRGVARRKDDHLIDETHDLNRKASLPHQENTDLYNKINLRQEN 181

QY 179 ELHKRIYETG-----PSGVNRE-----SPTPFNAFVETRDVQVLESLTPQ 222
 Db 182 LLRAKIAENERNPMSLMGSGSNYEQIMPPROTQOPF-----DSNRFOVAL Q 232
 QY 223 QNNIEPSTA---PKGLIQLT 239
 Db 233 PNNHHYSSAGREDOTALQTV 252

RESULT 6

AG_PETHY STANDARD: PRT: 242 AA.

ID AG_PETHY
 AC Q40885;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE AGAMOUS protein (PMADS3).
 GN AG1 OR MADS3.
 OS Petunia hybrida (Petunia).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eusterids I; Solanales; Solanaceae; Petunia.
 OC NCBI_TaxID=4102;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=flower;
 RA MEDLINE=94004017; PubMed=8104573;
 RX Tsuchimoto S., van der Krol A.R., Chua N.H.;
 RT "Ectopic expression of PMADS3 in transgenic petunia phenocopies the
 RL Petunia blind mutant.";
 RT Plant Cell 5:843-853(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, Mitchell;
 RA Takatsui H., Kapoor M.;
 RT "Silencing of PMADS3 affects floral organ and meristem identity in
 RL Petunia.";
 RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
 CC GENES THAT DETERMINE STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
 CC FLOWERS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN STAMENS AND CARPELS.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
 CC -----
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 CC -----
 DR EMBL: X72912; CAAS1417.1; -;
 DR EMBL: AB076051; BAB79434.1; -;
 DR HSSP: P11746; 1NMN.
 DR TRANSFAC: T03135; -;
 DR Mendel: 9809; Pethy:MADS.8.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS00350; MADS_BOX_2; 1.
 DR PROSITE: PS00350; MADS_BOX_3; 1.
 DR Transcription regulation; DNA-binding; Activator; Nuclear protein.
 FT DOMAIN 19 73 MADS.
 FT DOMAIN 112 184 K-BOX.

SQ SEQUENCE 242 AA: 27907 MW: A5249306B807A6BD CRC64:
 Query Match 34.3%; Score 417.5; DB 1; Length 242;
 Best Local Similarity 39.7%; Pred. No. 5e-21;
 Matches 96; Conservative 50; Mismatches 73; Indels 23; Gaps 6;

QY 1 MGRGKIVIRIDNSTSRQVTFKRRNGJFKKAKELAIICDAEVLGVTSSGRLEYSSST 60
 Db 17 LGRGKLEIRLENTTNRQVTFCKRRNGLLKAYELSLVLCDEVALITVSSGRLEYAVANN 76
 QY 61 SMKSVYDRYGAKEEQDQ--VVANPNSELKEMOREAASLRQOLHNLQENYQLTGDDLSG 117
 Db 77 SVKATIERKAKCSDSNSTGSIAEANQ--YYQGEASKLRQIGLQNLQNNFLGESIAA 134
 QY 118 LNVKELQSIENOLETSLRGVRAKKDHLIDELHIDINRRASLFHOENDLVYKINLTQEN 177
 Db 135 LNLRLRLNLEOKIEKGIKRAKNELLFAETIYWMQR-----EIDLHN-----NN 180
 QY 178 DELHKRIYETGSPGVNRESPFPFNAFV---ETPDVQVLESLTPQNNIEPSTAPKL 234
 Db 181 QYLRKRIETENSQOMNL-MGSSSYDLVPPQGSFDARNYLVQVGLQTNHHYPRQDQPL 239
 QY 235 GL 236
 Db 240 QL 241

RESULT 7

AGL5_ARATH STANDARD: PRT: 246 AA.

ID AGL5_ARATH
 AC P29385;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Agamous-like MADS box protein AGL5.
 GN AGL5.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=91160981; PubMed=1672119;
 RA Ma H., Yanofsky M.F., Meyerowitz E.M.;
 RT "AGL1-AGL6, an Arabidopsis gene family with similarity to floral
 RL homeotic and transcription factor genes.";
 RL Genes Dev. 5:484-495(1991).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M55553; AAA32735.1; -;
 DR PIR: E39534; E39534.
 DR HSSP: P11746; 1NMN.
 DR TRANSFAC: T03028; -;
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.

DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 18 72 MADS.
 FT DOMAIN 111 183 K-BOX.
 SQ SEQUENCE 246 AA; 28157 MW; D4D59316D55606D9 CRC64;

Query Match 34.3%; Score 417; DB 1; Length 246;
 Best Local Similarity 38.7%; Pred. No. 5,5e-21;
 Matches 96; Conservative 53; Mismatches 73; Indels 26; Gaps 7;

QY 1 MGRGKIVIRIDNSTROYTFKRRNGIFKAKELALICDAEGLVTFSTGRLEYEST 60
 DB 16 IGRGKIEIKRIENTTNROYTFCKRRNGILKRAYELSVLCDAEVALVFTSRGRLEYEVANN 75
 QY 61 SMKSVIDRGKAKEEQVYANP-----NSELKFQREASLRQOLHNIOENYRQLTGDDLS 116
 DB 76 SVRGTEIRYKACSD--AVNPPTTEANIOYVOEASKLRQTRDIONLNRHILGESLG 132
 QY 117 GLNVEKLOSLNQLETSILRGYRARKDHLIDELHDLNRKASLPHOENTDLYNKI---NL 172
 DB 133 SLNFEELKLNLSRLKLGISRYRSKKHEMLVALEIYMQKREIELQNDMNYLRSKITEETGL 192
 QY 173 IROENDELHK-KIYETEGSPGVNRESPTFPNFAYVETRDVQVLELSTLPQONNIEPSTA 231
 DB 193 OOEESVTHOGVYES-GVTSOSHOGYRNRYVIANLLE-----PNQSSNODOP 241
 QY 232 PKLGQL 239
 DB 242 P---LQLV 246

RESULT 8

AG_PANGI STANDARD; PRT; 242 AA.
 AC Q40872;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE AGAMOUS protein (GAG2).
 GN AG2.
 OS Panax ginseng (Korean ginseng).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids II; Apiales; Araliaceae; Panax.
 OX NCBI_TaxID=4054;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Flower.
 RA Kim Y.S., Lee H.S., Hoon L.S., Yoo C.J., Chung W.L., Liu J.R.;
 RT "The cDNA sequence of two MADS box genes in Panax ginseng (GAG2, GAG3)."
 RL (in) Plant Gene Register PGR95-060.
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
 CC GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
 CC FLOWERS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: FLOWER. PREFERENTIALLY EXPRESSED IN STAMEN AND
 CC CARPEL AND WEAKLY IN PETAL. UNDETECTED IN LEAVES AND ROOTS.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
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CC EMBL; 246612; CAAB6585.1; -
 DR HSSP; P11746; 1KMN.
 DR TRANSFAC; T03099; -
 DR InterPro; IPR002487; K-box.
 DR InterPro; IPR002100; MADS-box.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TP; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Activator; Nuclear protein.
 FT DOMAIN 19 73 MADS.
 FT DOMAIN 112 184 K-BOX.
 SQ SEQUENCE 242 AA; 27781 MW; 0B3F02937B24CF76 CRC64;

Query Match 34.1%; Score 414.5; DB 1; Length 242;
 Best Local Similarity 38.8%; Pred. No. 7,9e-21;
 Matches 95; Conservative 48; Mismatches 77; Indels 25; Gaps 5;

QY 1 MGRGKIVIRIDNSTROYTFKRRNGIFKAKELALICDAEGLVTFSTGRLEYEST 60
 DB 17 IGRGKIEIKRIENTTNROYTFCKRRNGILKRAYELSVLCDAEVALVFTSRGRLEYEVANN 76
 QY 61 SMKSVIDRGKAKEEQVYANP-----SELKFQREASLRQOLHNIOENYRQLTGDD 114
 DB 77 SVRGTEIRYKACSD--SPNTSSVSANQFOYOEASKLRQELSSIQKNRMAGES 131
 QY 115 LSGLNVEKLOSLNQLETSILRGYRARKDHLIDELHDLNRKASLPHOENTDLYNKINILR 174
 DB 132 LGSLEYRDLKGLTETKLEKGISRYRSKKNELFALEIYMQKREIELHNNQYLRAKI---- 187
 QY 175 QENDELHKKIYETEGSPGVNRESPTFPNFAYVETRDVQVLELSTLPQONNIEPAPKL 234
 DB 188 AENERAQOQHNNLMPGSSDYELAPPOSF-----DGRNYIQLNGIQLPNHY--SRQDOT 237
 QY 235 GLQL 239
 DB 238 ALQDV 242

RESULT 9

AG_TOBAC STANDARD; PRT; 248 AA.
 AC Q43585;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE AGAMOUS protein (NAG1).
 GN AG1.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CY. SAMSUN. TISSUE=Stamen;
 RX MEDLINE=9412000; PubMed=7507255;
 RA Kempin S.A., Mandel M.A., Yanofsky M.F.;
 RT "Conversion of perianth into reproductive organs by ectopic
 RT expression of the tobacco floral homeotic gene NAG1."
 RL Plant Physiol. 103:1041-1046(1993).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
 CC GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
 CC FLOWERS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
 CC -----


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Query Match          33.3%; Score 405; DB 1; Length 248;
Best Local Similarity 43.9%; Pred. No.3,4e-20;
Matches    90; Conservative   42; Mismatches   55; Indels    18; Gaps      5

QY      1 MGGRGIYRIDNSTSQVTFESRRNGIFRKAKELALICDAEVLVFSSGRLYEYSST 60
DB       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Dd      16 LGRGIEIKRIEMTNTKRVQFCKRRNGLLKAKVELSVLCDAEVALVTFSTGRILEYANN 75
QY      61 SMKSYVIDPYCGAKEEQOVANPNPS----ELKFMOPRPAASLRQOHNLOENROLTGSDLS 116
DB       |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Dd      76 SVRGTEIRRYKKACSD---AVNPSPYTEANTQYYQDEASKLRQIDNSNRHIVGESLG 132
QY     117 GLNVKEQLSLLENQLETSLRGVRAKKDHLLIDEIHLNKRASLPHQENTDYLNKI----- 170
DB      133 SLNKEELKNEJREKLEKISVRFSKKNELLVALETVEYOKREMELQHNNMYLRAKTAFGARL 192
QY     171 NLIRENDDELH-KKIYFTBEGSGVN 194
Dd      193 NPDOGSSESVIGCTTYE---SGLVS 213

RESULT 12
AGL8_ARATH ID AGL8_ARATH STANDARD: PRT: 242 AA.
AC Q38876;
DT 15-DEC-1998 (Rel. 37, Created)
Dt 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
De Agamous-like MADS box protein AGL8.
OS AGL8 OR AT5G60910 OR MSJ3.3.
OC Arabidopsis thaliana (Mouse-ear cress).
CC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatops II; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC Eumastoid II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RP STRAIN-CV. COLUMBIA;
RC MEDLINE=96093419; PubMed=8535133;
RX Mandel M.A., Yanofsky M.F.;
RA "The Arabidopsis AGL8 MADS box gene is expressed in inflorescence
RT meristems and is negatively regulated by APETALA1.";
RL Plant Cell 7:1763-1771(1995).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN-CV. COLUMBIA;
RC MEDLINE=98162728; PubMed=9501997;
RX Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
RA Tabata S.;
RA "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT Sequence features of the regions of 1,191,918 bp covered by seventeen
RL physically assigned pl clones.";
RL DNA Res. 4:401-414(1997).
CC -|- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -|- SUBCELLULAR LOCATION: Nuclear (by similarity).
CC -|- DEVELOPMENTAL STAGE: DRAMATICALLY UP-REGULATED UPON THE TRANSITION
CC FROM VEGETATIVE TO REPRODUCTIVE DEVELOPMENT, WHERE ITS EXPRESSION
CC IS DETECTED IN CAULINE LEAVES, STEMS, AND IN FLOWERS.
CC -|- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -|- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
CC SRP-TYPE TRANSCRIPTION FACTORS (K-BOX).
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CC CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC      -----
CC CC      [1] NCBI_TaxID=3728;
CC OC       Sinapis alba (white mustard) (Brassicaceae; Sinapnits.
CC OS       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC OC       Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC OC       eurostids II; Brassicales; Brassicaceae; Sinapnits.
CC XX       [1]
CC RN       SEQUENCE FROM N.A.
CC RP       TISSUE=Flower;
CC RC       MEDLINE=97077349; Pubmed=8919916;
CC RX       Menzel G., Apel K., Melzer S.;
CC RA       "Identification of two MADS box genes that are expressed in the
CC RT       apical meristem of the long-day plant Sinapis alba in transition to
CC RT       flowering."
CC RL       Plant J. 9:399-408(1996).
CC CC       -|- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC CC       -|- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC CC       -|- DEVELOPMENTAL STAGE: EXPRESSED IN APICAL MERISTEMS IN TRANSITION
CC CC       TO FLOWERING.
CC CC       -|- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC CC       FACTORS.
CC CC       -|- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
CC CC       SRP-TYPE TRANSCRIPTION FACTORS (K-BOX).
CC CC       -----
```

US Lycopersicon esculentum (Tomato).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
CC NCBI_TaxID=4081,
RX [1]
RR
RP SEQUENCE FROM N.A.
RC STRAIN=CV_VENT CHERRY; TISSUE=FloWer;
RX MEDLINE=93251098; PubMed=1688249;
RA Punell L., Abu-Abeid M., Zamir D., Nacken W., Schwarz-Sommer Z.,
RA Lifschitz E.;
RT "The MAD5 box gene family in tomato: temporal expression during
RT floral development, conserved secondary structures and homology with
RRL homeotic genes from Antirrhinum and Arabidopsis.";
RRL Plant J. 1:255-266(1991).
CC -I- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -I- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -I- TISSUE SPECIFICITY: FLOWER-SPECIFIC.
CC -I- SIMILARITY: BELONGS TO THE MAD5 DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.

CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
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 CC -----
 CC EMBL: X60757; CAA43169.1; -
 CC HSSP: P11831; 1SR5.
 CC TRANSFAC: T03186; -
 CC InterPro: IPR002487; K-box.
 CC InterPro: IPR002100; MADS-box.
 CC Pfam: PF01486; K-box; 1.
 CC Pfam: PF00319; SRF-TE; 1.
 CC PRINTS: PR00404; MADSDOMAIN.
 CC SMART: SM00432; MADS_1.
 CC PROSITE: PS00350; MADS_BOX_1; 1.
 CC PROSITE: PS50066; MADS_BOX_2; 1.
 CC Transcription regulation; DNA-binding; Nuclear protein.
 CC KW DOMAIN 3 57 MADS.
 CC FT DOMAIN 97 169 K-BOX.
 CC SEQUENCE 227 AA; 26403 MW; 4976195B3BDE53F5 CRC64;

Query Match 31.8%; Score 386.5; DB 1; Length 227;
 Best Local Similarity 36.8%; Pred. No. 5; Le-19;
 Matches 81; Conservative 58; Mismatches 58; Indels 23; Gaps 5;

QY 1 MGKRTIVIRINDNSTSRQVTFKRRNGIFKAKELALTCDAEVLGVFFSGTGLVEYST 60
 DB 1 MGRGVOLIKREKINQVTFKRRSGDLKKAHEISVLCDAEVLGVFFSGTGLVEYAND 60
 QY 61 S-MKSVTDTRYGK-AKEEDQVAVANPNSSEIKFQREASLRQOLHNLQENTYRLTGDDSL 118
 DB 61 SCMERILERYRYSFARQKOLVPTDHTSPVSTLEHRLKARLEVLQKNQHYGDELSL 120
 QY 119 NKEILOSLENOLETSLRGVRAKKDHLIDELHDLNRKASLPHOENTDLYNKINLIROEND 178
 DB 121 SMKEIOLNLEHOLDALKHIRSKNQLM-----HESISVLQKKRALDLOHNN 166
 QY 179 ELHKIYETEGP-----SGVNRES---PFPNFAVETRDV 211
 DB 167 QLSKKVKEKESAOQISGINSSSLFAHIDFLITGYSTNV 206

RESULT 15
 JOIN_LYCES
 ID JOIN_LYCES STANDARD; PRT; 265 AA.
 AC Q9F016;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE MADS-box JOINTLESS protein (LemDS).
 GN J.
 OS Lycopersicon esculentum (Tomato).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 CC NCBI_Taxid=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Heinz 1706;
 RX MEDLINE=20426111; PubMed=10972295;
 RA Mao L., Begum D., Chuang H.W., Budiman M.A., Szymkowiak E.J.,
 RA Irish E.F., Wing R.A.;
 RT "JOINTLESS is a MADS-box gene controlling tomato flower abscission
 RT zone development.";
 RL Nature 406:910-913(2000).
 CC -1- FUNCTION: PUTATIVE TRANSCRIPTION FACTOR THAT COORDINATES GENE

CC EXPRESSION UNDERLYING THE DIFFERENTIATION OF THE PEDICEL
 CC ABSCISSION ZONE. MAY ALSO BE INVOLVED IN THE MAINTENANCE OF THE
 CC INFLORESCENCE MERISTEM STATE.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN SHOOT
 CC TIPS AND AXILLARY BUDS. ALSO FOUND IN FULLY DEVELOPED PEDICELS AND
 CC FLOWERS.
 CC -1- BIOTECHNOLOGY: Mutation in 'JOINTLESS' yields 'stemless' tomato
 CC fruits which are widely used in the processing tomato industry.
 CC The fruits support mechanical harvesting and are not subject to
 CC physical wounding during transportation.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS 1 PROBABLE DIMERIZATION DOMAIN FOUND IN SRF-
 CC TYPE TRANSCRIPTION FACTORS (K-BOX).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF275345; AAC09811.1; -
 CC InterPro: IPR002487; K-box.
 CC InterPro: IPR002100; MADS-box.
 CC Pfam: PF01486; K-box; 1.
 CC Pfam: PF00319; SRF-TE; 1.
 CC PRINTS: PR00404; MADSDOMAIN.
 CC SMART: SM00432; MADS_1.
 CC PROSITE: PS00350; MADS_BOX_1; 1.
 CC PROSITE: PS50066; MADS_BOX_2; 1.
 CC Transcription regulation; DNA-binding; Developmental protein;
 CC KW Nuclear protein.
 CC FT DOMAIN 3 57 MADS.
 CC FT DOMAIN 59 173 K-BOX.
 CC FT DOMAIN 58 61 POLY-SER.
 CC FT DOMAIN 176 183 POLY-ASN.
 CC FT DOMAIN 200 204 POLY-ASN.
 CC SEQUENCE 265 AA; 30426 MW; EB687F9DD9DC1B5D CRC64;

Query Match 31.7%; Score 386; DB 1; Length 265;
 Best Local Similarity 37.5%; Pred. No. 6; Le-19;
 Matches 96; Conservative 45; Mismatches 77; Indels 38; Gaps 6;

QY 1 MGKRTIVIRINDNSTSRQVTFKRRNGIFKAKELALTCDAEVLGVFFSGTGLVEYST 60
 DB 1 MAREKIQIKRKINDSTARQVTFKRRRGLFKKAELSVLCDAVALLIFSSGKLDYSSS 60
 QY 61 SKSVTDTRYGKAKEEQVAVANPNSSEIKF-----MREASLRQOLHNLQENTYRLTGDDL 115
 DB 61 SMKQILERRDHSKNELEKIDPSLEQLVENSYSRLSEIKSHRL-----RQMRGSEL 116
 QY 116 SCINVELOSLENOLETSLRGVRAKKDHLIDELHDLNRKASLPHOENTDLYNKINLIRO 175
 DB 117 OGNIIELOOLESTETGSLRVIERKGDKIMREINLOQKGNHLENEKRLQYQWESIN 176
 QY 176 END-----ELHKIYETE-----GPSGVNRESPT-PFPNFAVETRDVQLESLTL 220
 DB 177 NNNNNNNGRGAGVAVFFEEENGFNNNNNNDDGSSSEVTPNCST-----DP 222
 QY 221 POONNTEPSTAPKGL 236
 DB 223 PRODDDSSTSLKGL 238

Search completed: August 11, 2002, 09:45:11
 Job time: 502 sec